

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 14, 2006, 19:51:35 ; Search time 29.5576 Seconds
(without alignments)
4176.460 Million cell updates/sec

Title: US-10-619-359A-4
Perfect score: 6443
Sequence: 1 MDLEGRNGGAENKFFKLN.....LAQGIYFMSVQAGAKRQ 1283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 80.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 6312.5 | 96.4 | 1280 | 1 DVHUI | multidrug resist |
| 2 | 5693 | 88.4 | 1276 | 1 DVHYIC | multidrug resist |
| 3 | 5677.5 | 88.1 | 1276 | 2 A34786 | multidrug resist |
| 4 | 5303.5 | 82.3 | 1276 | 1 DVMS1 | multidrug resist |
| 5 | 5230 | 81.2 | 1277 | 2 JH0502 | p-glycoprotein - r |
| 6 | 5032 | 78.1 | 1104 | 1 DVMS1A | multidrug resist |
| 7 | 4953 | 76.9 | 1279 | 1 DVHUS | multidrug resist |
| 8 | 4872.5 | 75.6 | 1276 | 1 DVMS2 | multidrug resist |
| 9 | 4866 | 75.5 | 1281 | 2 T48123 | p-glycoprotein iso |
| 10 | 4838.5 | 75.1 | 1278 | 2 S41646 | p-glycoprotein - r |
| 11 | 4430.5 | 68.8 | 1287 | 2 S55692 | multidrug resist |
| 12 | 3238.5 | 50.3 | 1321 | 2 T42228 | p-glycoprotein sis |
| 13 | 3234.5 | 50.2 | 1321 | 2 T42842 | bile salt transpor |
| 14 | 2892 | 44.9 | 1294 | 2 T19982 | hypothetical prote |
| 15 | 2846.5 | 44.2 | 1289 | 2 D87789 | protein C3466.4 [i |
| 16 | 2832.5 | 44.0 | 1275 | 2 T31073 | multidrug resist |
| 17 | 2756.5 | 42.8 | 1321 | 2 T23476 | hypothetical prote |
| 18 | 2754.5 | 42.8 | 1321 | 2 S27337 | multidrug resist |
| 19 | 2714.5 | 42.1 | 655 | 1 DVHY2C | multidrug resist |
| 20 | 2658 | 41.3 | 1283 | 2 A47377 | multidrug resist |
| 21 | 2640 | 41.0 | 1286 | 2 T02187 | probable ABC trans |
| 22 | 2639.5 | 41.0 | 1292 | 2 T48007 | p-glycoprotein hom |
| 23 | 2602.5 | 40.4 | 1278 | 2 E86155 | probable ABC trans |
| 24 | 2574.5 | 40.0 | 1302 | 2 A41249 | multidrug resist |
| 25 | 2543.5 | 39.5 | 1229 | 2 D85023 | p-glycoprotein-lik |
| 26 | 2540.5 | 39.4 | 1229 | 2 T52319 | p-glycoprotein-lik |
| 27 | 2531.5 | 39.3 | 1230 | 2 E85023 | probable P-glycopr |
| 28 | 2511.5 | 39.0 | 1229 | 2 P86155 | probable ABC trans |
| 29 | 2482.5 | 38.5 | 1302 | 2 B41249 | multidrug resist |

ALIGNMENTS

RESULT 1

DVHUI multidrug resistance protein 1 - human

N; Alternate names: P-glycoprotein 1

C; Species: Homo sapiens (man)

C; Date: 31-Dec-1990 #sequence revision 18-Aug-1995 #text change 09-Jul-2004

C; Accession: A34914; PS0162; S15500; A25059; S43838; I52238; I65204

R; Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.

J. Biol. Chem. 265, 506-514, 1990

A; Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin

A; Reference number: A34914; MUID:90094448; PMID:1967175

A; Accession: A34914

A; Molecule type: DNA

A; Residues: 1-1280 <CH>

A; Cross-references: UNIPROT:P08183; UNIPARC:UPI000003BD16; GB:M29447; GB:J05168; NID:G1

R; Kioka, N.; Yamano, Y.; Komano, T.; Ueda, K.

submitted to JIPID, April 1991

A; Reference number: PS0162

A; Accession: PS0162

A; Molecule type: DNA

A; Residues: 1-22 <KIO>

A; Cross-references: UNIPARC:UPI00001746C8

R; Kioka, N.; Yamano, Y.; Komano, T.; Ueda, K.

submitted to the EMBL Data Library, April 1991

A; Description: Transcriptional regulation of multidrug resistance gene (MDR1) expression

A; Reference number: S15500

A; Accession: S15500

A; Molecule type: DNA

A; Residues: 1-22, 'R' <KI2>

A; Cross-references: UNIPARC:UPI000016AD22; EMBL:X58723; NID:G34522; PIDN:CAA41558.1; PI

R; Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I

Cell 47, 381-389, 1986

A; Title: Internal duplication and homology with bacterial transport proteins in the mdr

A; Reference number: A25059; MUID:87028230; PMID:2876781

A; Accession: A25059

A; Molecule type: mRNA

A; Residues: 1-184, 'V', 186-1280 <CH2>

A; Cross-references: UNIPARC:UPI0000039699; GB:M14758; NID:G187468; PIDN:AAA59575.1; PID

R; Chambers, T.C.; Pohl, J.; Gläse, D.B.; Kuo, J.F.

Biochem. J. 299, 303-315, 1994

A; Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase of

A; Reference number: S43838; MUID:94220047; PMID:7909431

A; Accession: S43838

A; Molecule type: protein

A; Residues: 656-689 <CHA>

A; Cross-references: UNIPARC:UPI00001746C9

R; Gekeler, V.; Weger, S.; Probst, H.

Biochem. Biophys. Res. Commun. 169, 796-802, 1990

A; Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li

A; Reference number: I52238; MUID:90290529; PMID:1972623

A; Accession: I52238

A; Status: translated from GB/EMBL/DBJ

hypothetical prote
multidrug resist
multidrug resist
P-glycoprotein pgp
hypothetical prote
multidrug resist
hypothetical prote
hypothetical prote
P-glycoprotein C -
hypothetical prote
P-glycoprotein 2 -
multidrug resist
multidrug resist
leptomycin B resis
hypothetical prote
hypothetical prote
probable P-glycopr

| Query Match | 96.4%; | Score 6212.5; | DB 1; | Length 1280; |
|-----------------------|--|----------------|-----------|--------------|
| Best Local Similarity | 96.5%; | Pred. No. 0; | | |
| Matches 1238; | Conservative 18; | Mismatches 24; | Indels 3; | Gaps 1; |
| 1 | MDLEGRNGAEGAKCNFFKLNKNSKODKGRKPTVSVFSMFRYSNWLDKLYVMVGTILAAII | 60 | | |
| 1 | MDLEGRNGAEGAKCNFFKLNKNSKODKGRKPTVSVFSMFRYSNWLDKLYVMVGTILAAII | 60 | | |
| 61 | HGAGLPLMLVFGDMTDTFANAGNLGDGALLFNNTSSNITUTVPMLEEDMTYAYY | 120 | | |
| 61 | HGAGLPLMLVFGDMTDTFANAGNLGDGALLFNNTSSNITUTVPMLEEDMTYAYY | 117 | | |
| 121 | YSGIGAGVLVAAYIOVSFWCLAGROIHRIKQOFFHAIIMROEIGWFDVHDVGEINRLTLD | 180 | | |
| 118 | YSGIGAGVLVAAYIOVSFWCLAGROIHRIKQOFFHAIIMROEIGWFDVHDVGEINRLTLD | 177 | | |
| 181 | DVSKINEGIGDKIGMFQSQMATEPFTGFIUGFTGKWLTLVILAIISPVLGLSAVAWAKILS | 240 | | |
| 178 | DVSKINEGIGDKIGMFQSQMATEPFTGFIUGFTGKWLTLVILAIISPVLGLSAVAWAKILS | 237 | | |
| 241 | SFTDKELLAYAKAGAAVEEVLAAIRTVIAPGGQKELERNYNLEBAKIGIKKAITANI | 300 | | |
| 238 | SFTDKELLAYAKAGAAVEEVLAAIRTVIAPGGQKELERNYNLEBAKIGIKKAITANI | 297 | | |
| 301 | STGAAPLLIYASVALAFWGTITVLVSKEYSIGQVLTVFFSVLIGAFSVGQASPSIAPAN | 360 | | |
| 298 | SIGAAPLLIYASVALAFWGTITVLVSKEYSIGQVLTVFFSVLIGAFSVGQASPSIAPAN | 357 | | |
| 361 | ARGAAPEIFKI INDKPSIDISYSKSHKPDNI KGNLAFRNVPSPSRKEVKILKGLNKLKV | 420 | | |
| 358 | ARGAAPEIFKI INDKPSIDISYSKSHKPDNI KGNLAFRNVPSPSRKEVKILKGLNKLKV | 417 | | |
| 421 | QSGQITVALVGNSCGKSTTVOLMORLYDPTPEGMVSDGQDIRTINVRFLREIIGVVSQEP | 480 | | |
| 418 | QSGQITVALVGNSCGKSTTVOLMORLYDPTPEGMVSDGQDIRTINVRFLREIIGVVSQEP | 477 | | |
| 481 | VLFPATTIAENIRYGREDTVMTDETEKAVKEANAYDFIMKLPQKFTDLVGERGAQLSGGQKQ | 540 | | |
| 478 | VLFPATTIAENIRYGREDTVMTDETEKAVKEANAYDFIMKLPQKFTDLVGERGAQLSGGQKQ | 537 | | |

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 14, 2006, 19:51:35 ; Search time 29.5576 Seconds
(without alignments)
4176.460 Million cell updates/sec

Title: US-10-619-359A-4
Perfect score: 6443
Sequence: 1 MDLEGRNGAENKFFKLN.....LAQGIYFMSVQAGKQ 1283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | ID | Description |
|------------|--------|-------|-------|--------|--------|--------------------|
| 1 | 6212.5 | 96.4 | 1280 | 1 | DVHUI | multidrug resist |
| 2 | 5693 | 88.4 | 1276 | 1 | DVH1C | multidrug resist |
| 3 | 5677.5 | 88.1 | 1276 | 2 | A34786 | multidrug resist |
| 4 | 5303.5 | 82.3 | 1276 | 1 | DVMS1 | multidrug resist |
| 5 | 5230 | 81.2 | 1277 | 2 | DVMS2 | p-glycoprotein - r |
| 6 | 5032 | 78.1 | 1104 | 1 | DVMS1A | multidrug resist |
| 7 | 4953 | 76.9 | 1279 | 1 | DVMS3 | multidrug resist |
| 8 | 4872.5 | 75.6 | 1276 | 1 | DVMS2 | multidrug resist |
| 9 | 4866 | 75.5 | 1281 | 2 | I48123 | p-glycoprotein iso |
| 10 | 4838.5 | 75.1 | 1278 | 2 | I48146 | p-glycoprotein - r |
| 11 | 4430.5 | 68.8 | 1287 | 2 | S55692 | multidrug resist |
| 12 | 4238.5 | 50.3 | 1321 | 2 | T42228 | p-glycoprotein sis |
| 13 | 3234.5 | 50.2 | 1321 | 2 | T42842 | bile salt transpor |
| 14 | 2892 | 44.9 | 1294 | 2 | T19882 | hypothetical prote |
| 15 | 2846.5 | 44.2 | 1289 | 2 | D87789 | protein C34G6.4 [i |
| 16 | 2832.5 | 44.0 | 1275 | 2 | T31073 | multidrug resist |
| 17 | 2756.5 | 42.8 | 1321 | 2 | T23476 | hypothetical prote |
| 18 | 2754.5 | 42.8 | 1321 | 2 | D27337 | multidrug resist |
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| 20 | 2658 | 41.3 | 1283 | 2 | A47377 | multidrug resist |
| 21 | 2640 | 41.0 | 1286 | 2 | T02187 | probable ABC trans |
| 22 | 2639.5 | 41.0 | 1292 | 2 | T48007 | P-glycoprotein hom |
| 23 | 2602.5 | 40.4 | 1278 | 2 | E86155 | probable ABC trans |
| 24 | 2574.5 | 40.0 | 1302 | 2 | A41249 | multidrug resist |
| 25 | 2543.5 | 39.5 | 1229 | 2 | D85023 | P-glycoprotein-lik |
| 26 | 2540.5 | 39.4 | 1229 | 2 | T52319 | P-glycoprotein-lik |
| 27 | 2531.5 | 39.3 | 1230 | 2 | E85023 | probable P-glycopr |
| 28 | 2511.5 | 39.0 | 1229 | 2 | F86155 | probable ABC trans |
| 29 | 2482.5 | 38.5 | 1302 | 2 | B41249 | multidrug resist |

| | | | | | | |
|----|--------|------|------|---|--------|--------------------|
| 30 | 2467 | 38.3 | 1323 | 2 | H85202 | hypothetical prote |
| 31 | 2447 | 38.0 | 1408 | 2 | T43261 | multidrug resist |
| 32 | 2419.5 | 37.6 | 1310 | 2 | S30328 | multidrug resist |
| 33 | 2417.5 | 37.5 | 1286 | 2 | A42150 | P-glycoprotein ppp |
| 34 | 2416 | 37.5 | 1268 | 2 | T22094 | hypothetical prote |
| 35 | 2413.5 | 37.5 | 1302 | 2 | S30327 | multidrug resist |
| 36 | 2412 | 37.4 | 1266 | 2 | T22090 | hypothetical prote |
| 37 | 2363 | 36.7 | 1254 | 2 | S27338 | P-glycoprotein C - |
| 38 | 2361 | 36.6 | 1222 | 2 | T14805 | hypothetical prote |
| 39 | 2314.5 | 35.9 | 1233 | 2 | T04251 | P-glycoprotein 2 - |
| 40 | 2300 | 35.7 | 1254 | 2 | T30855 | multidrug resist |
| 41 | 2290.5 | 35.6 | 1307 | 2 | T30882 | multidrug resist |
| 42 | 2279.5 | 35.4 | 1362 | 2 | T41534 | leptomycin B resis |
| 43 | 2273 | 35.3 | 1318 | 2 | T21266 | hypothetical prote |
| 44 | 2238.5 | 34.7 | 1327 | 2 | T21268 | hypothetical prote |
| 45 | 2228 | 34.6 | 1245 | 2 | G86404 | probable P-glycopr |

ALIGNMENTS

RESULT 1

DVHUI
multidrug resistance protein 1 - human
N:Alternate names: P-glycoprotein 1
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence revision 18-Aug-1995 #text change 09-Jul-2004
A:Accession: A34914; PS0162; S15500; A25059; S43838; I52238; I52238; I52238
R:Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.
J. Biol. Chem. 265, 506-514, 1990
A:Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin
A:Reference number: A34914; MUID:90094448; PMID:1967175
A:Accession: A34914
A:Molecule type: DNA
A:Residues: 1-1280 <CHE>
A:Cross-references: UNIPROT:P08183; UNIPARC:UPI000003BD16; GB:M29447; GB:J05168; NID:gl
R:Kioka, N.; Yamano, Y.; Komano, T.; Ueda, K.
submitted to JIPID, April 1991
A:Reference number: PS0162
A:Accession: PS0162
A:Molecule type: DNA
A:Residues: 1-22 <KIO>
A:Cross-references: UNIPARC:UPI00001746C8
R:Kioka, N.; Yamano, Y.; Komano, T.; Ueda, K.
submitted to the EMBL Data Library, April 1991
A:Description: Transcriptional regulation of multidrug resistance gene (MDR1) expressio
A:Reference number: S15500
A:Accession: S15500
A:Molecule type: DNA
A:Residues: 1-22, 'R' <K12>
A:Cross-references: UNIPARC:UPI000016AD22; EMBL:X58723; NID:G34522; PIDN:CAA41558.1; PI
R:Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I
Cell 47, 381-389, 1986
A:Title: Internal duplication and homology with bacterial transport proteins in the mdr
A:Reference number: A25059; MUID:87028230; PMID:2876781
A:Accession: A25059
A:Molecule type: mRNA
A:Residues: 1-184, 'V', 186-1280 <CH2>
A:Cross-references: UNIPARC:UPI0000039699; GB:M14758; NID:gl87468; PIDN:AAA59575.1; PID
R:Chambers, T.C.; Pohl, J.; Glass, D.B.; Kuo, J.F.
Biochem. J. 299, 309-315, 1994
A:Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase of
A:Reference number: S43838; MUID:94220047; PMID:7909431
A:Accession: S43838
A:Molecule type: protein
A:Residues: 656-689 <CHA>
A:Cross-references: UNIPARC:UPI00001746C9
R:Geleler, V.; Weger, S.; Probst, H.
Biochem. Biophys. Res. Commun. 169, 796-802, 1990
A:Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li
A:Reference number: I52238; MUID:90290529; PMID:1972623
A:Accession: I52238
A>Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 178-215 <RES>
 A;Cross-references: UNIPARC:UPI000016A03C; GB:M37724; NID:G183537; PIDN:AAA88047.1; PID:
 A;Accession: 165204
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 800-856 <RE2>
 A;Cross-references: UNIPARC:UPI000016A03D; GB:M37725; NID:G183538; PIDN:AAA88048.1; PID:
 C;Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
 C;Genetics:
 A;Gene: GDB:PCYL1; MDR1
 A;Cross-references: GDB:120712; OMIM:171050
 A;Map position: 7q21-7q21
 A;Superfamily: multidrug resistance protein; ATP-binding cassette homology
 C;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;
 F:1-638,653-1280/Region: duplication
 F:49-350/Domain: hydrophobic <HB1>
 F:351-637/Domain: hydrophobic <HB1>
 F:410-604/Domain: ATP-binding cassette homology <ABC1>
 F:427-434/Region: nucleotide-binding motif A (P-loop)
 F:551-555/Region: nucleotide-binding motif B
 F:638-708/Domain: linker <LIN>
 F:709-993/Domain: hydrophobic <HB2>
 F:994-1280/Domain: hydrophobic <HB2>
 F:1053-1249/Domain: ATP-binding cassette homology <ABC2>
 F:1070-1077/Region: nucleotide-binding motif A (P-loop)
 F:1198-1200/Region: nucleotide-binding motif B
 F:91,94,99/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:433/Binding site: ATP (Lys) #status predicted
 F:661,667,671/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status exp
 F:667,671,683/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status
 F:1076/Binding site: ATP (Lys) #status predicted

Query Match 96.4%; Score 6212.5; DB 1; Length 1280;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 1238; Conservative 18; Mismatches 24; Indels 3; Gaps 1;

QY 1 MLEGDRNGAEGKKNFFKLNKSKKKKKKPTVSVFSPRYGNWLDKLMVVGTLAAII 60
 DB 1 MLEGDRNGAEGKKNFFKLNKSKKKKKKPTVSVFSPRYGNWLDKLMVVGTLAAII 60
 QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAYV 120
 DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAYV 117
 QY 121 YSGIGAGVLVAAYIQVSWFCLAAAGROHKIRKQFFHAIHQEIGWDFDHDVDELNRLTD 180
 DB 118 YSGIGAGVLVAAYIQVSWFCLAAAGROHKIRKQFFHAIHQEIGWDFDHDVDELNRLTD 177
 QY 181 DYSKINEGIDKGMFQSMATPFTGTVGFTGKWLTLVLAISPVGLSAAVWAKILS 240
 DB 178 DYSKINEGIDKGMFQSMATPFTGTVGFTGKWLTLVLAISPVGLSAAVWAKILS 237
 QY 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAPGGOKKELERKNNLEAKRIGIKKAITANI 300
 DB 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAPGGOKKELERKNNLEAKRIGIKKAITANI 297
 QY 301 SIGAFLLIYASALAFWYGTTLVLSEKSYIGQVLTVFFSVLIGAFSGVQASPSIEAFAN 360
 DB 298 SIGAFLLIYASALAFWYGTTLVLSEKSYIGQVLTVFFSVLIGAFSGVQASPSIEAFAN 357
 QY 361 ARGAAFEIKIDNKPISDSYSGKSHKPNKGNLBNVHPSYPSRKEVKILKGNLKV 420
 DB 358 ARGAAFEIKIDNKPISDSYSGKSHKPNKGNLBNVHPSYPSRKEVKILKGNLKV 417
 QY 421 QSGQTVLVNGSGCGSTTVLMORLYDPTGVMVSDGQDITNVRFLREIIGVVSQEP 480
 DB 418 QSGQTVLVNGSGCGSTTVLMORLYDPTGVMVSDGQDITNVRFLREIIGVVSQEP 477
 QY 481 VLFATTIAENIRYGRDVTWDETEKAVKEANAYDFIMKLPKQFDTLVGERGQALSGGQK 540
 DB 478 VLFATTIAENIRYGRDVTWDETEKAVKEANAYDFIMKLPKQFDTLVGERGQALSGGQK 537

RESULT 2

DHYIC

multidrug resistance protein 1 - Chinese hamster

N/Alternate names: P-glycoprotein pgp1

C/Species: Crictetus griseus (Chinese hamster)

C/Date: 31-Dec-1990 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C/Accession: A38696; B38696; A27126; S33768; I52823

R/Deviator: S.E.; Hussain, A.; Davide, J.P.; Melera, P.W.

J. Biol. Chem. 266, 4545-4555, 1991

A/Title: Full length and alternatively spliced pgp-1 transcripts in multidrug-resistant

A/Reference number: A38696; MUID:91154265; PMID:1671863

A/Accession: A38696

A/Molecule type: mRNA

A/Residues: 1-1276 <DEV>

A/Cross-references: UNIPROT:P21448; UNIPARC:UPI000004FE21; GB:M59253; NID:G191154; PIDN

A/Molecule type: mRNA

A/Accession: C38696

A/Residues: 108-1276 <DE1>

A/Cross-references: UNIPARC:UPI000008B642; GB:M59254; NID:G191156; PIDN:AAA37005.1; PID

A;Experimental source: clone ADX185
 A;Accession: B38696
 A;Molecule type: mRNA
 A;Residues: 1-32,771-1276 <DE2>
 A;Cross-references: UNIPARC:UPI000000663F; GB:M59252; NID:g191152; PIDN:AAA37003.1; PID:
 R;Endicott, J.A.; Juranaka, P.F.; Sarangi, F.; Gerlach, J.H.; Deuchars, K.L.; Ling, V.
 Mol. Cell. Biol. 7, 4075-4081, 1987
 A;Title: Simultaneous expression of two P-glycoprotein genes in drug-sensitive Chinese h
 A;Reference number: A27126; MUID:86121232; PMID:2893255
 A;Accession: A27126
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 706-1276 <END>
 A;Cross-references: UNIPARC:UPI0000170730; GB:M17897; NID:g191158; PIDN:AAA37006.1; PID:
 R;Zastawny, R.L.; Ling, V.
 Biochim. Biophys. Acta 1173, 303-313, 1993
 A;Title: Structural and functional analysis of 5' flanking and intron 1 sequences of the
 A;Reference number: S33768; MUID:93305724; PMID:8100449
 A;Accession: S33768
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-21 <ZAS>
 A;Cross-references: UNIPARC:UPI00001746CA; EMBL:L03286
 R;Teeter, L.D.; Eckersberg, T.; Tsai, Y.; Kuo, M.T.
 Cell Growth Differ. 2, 429-437, 1991
 A;Title: Analysis of the Chinese hamster P-glycoprotein/multidrug resistance gene pgp1
 A;Reference number: I52823; MUID:92089970; PMID:1661134
 A;Accession: I52823
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-21 <RES>
 A;Cross-references: UNIPARC:UPI00001746CA; GB:881975; NID:g240862
 C;Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
 structurally and functionally unrelated lipophilic antitumor drugs.
 C;Genetics:
 A;Gene: pgp1
 C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
 C;Keywords: alternative splicing; ATP; duplication; glycoprotein; nucleotide binding; P-
 F;407-601/Domain: ATP-binding cassette homology <ABC1>
 F;424-431/Region: nucleotide-binding motif A (P-loop)
 F;548-552/Region: nucleotide-binding motif B
 F;1050-1246/Domain: ATP-binding cassette homology <ABC2>
 F;1067-1074/Region: nucleotide-binding motif A (P-loop)
 F;1193-1197/Region: nucleotide-binding motif B
 F;87,91,96/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;430/Binding site: ATP (Lys) #status predicted
 F;1073/Binding site: ATP (Lys) #status predicted
 Query Match 88.4%; Score 5693; DB 1; Length 1276;
 Best Local Similarity 86.7%; Pred. No. 1.7e-312;
 Matches 1112; Conservative 89; Mismatches 75; Indels 6; Gaps 3;
 QY 1 MDLEGRNGAGKKNFKLNKSKDKKPKVSPSPRYSNMLDKLMMVGTAAII 60
 DB 1 MFEEDFS-GRKDKFLKGRKSKKSKKPKVSVFTMFYAGWLDRLMLVGTAAII 59
 QY 61 HGAGLPMLLVFGDMTDTFANAGNLGDLGALLFNNTNNSNITDTPVMNLEEDTRYAY 120
 DB 60 HGVALPMLLVFGDMTDSFASVGNIPFNAT--NNATQVNASDI FG--KLEEMTYAY 114
 QY 121 YSGIGAGLVAAIYQVSWFCLAAAGROHKIRKQFPHAIMKROEIGWDFDHDVGLNTRLTD 180
 DB 115 YTGIGAGLVIAIYQVSWFCLAAAGROHKIRKQFPHAIMKROEIGWDFDHDVGLNTRLTD 174
 QY 181 DVSKNEGIGDKIMFGFQSNATPFTCTGIVGTGKTLTVILALISPVGLSAAVWAKILS 240
 DB 175 DVSKNEGIGDKIMFGFQSNATPFTCTGIVGTGKTLTVILALISPVGLSAGIWAIIIS 234
 QY 241 SPTDKELAYAKAGAAVEEVLAAIRTVIAFGGOKKELRYNNKLEBAKIGIKKAITANI 300
 DB 235 SPTDKELQAYAKAGAAVEEVLAAIRTVIAFGGOKKELRYNNKLEBAKIGIKKAITANI 294

QY 301 SIGNAPELLIYASALAPFWYGTTLVLSEYISIGQVLTIVFFSVLIGAPSVGQASPSIEAFAN 360
 DB 295 SMGAAPLLIYASALAPFWYGTSLVISEYISIGQVLTIVFFFAVLIAFPFSGOASPNEAFAN 354
 QY 361 ARGAAPEIFKIIDNKPSIDISYSGHGKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
 DB 355 ARGAAPEIFNIIDNKPSIDISYSGHGKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 414
 QY 421 QSGQTVALVGNSSCGSKSTTVQLMORLYDPTPEGMVSDGDQIRTNVRFLEIIGVVSQEP 480
 DB 415 QSGQTVALVGNSSCGSKSTTVQLMORLYDPTPEGMVSDGDQIRTNVRFLEIIGVVSQEP 474
 QY 481 VLPATTIAENIRYGRDVTWDETEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGQKQ 540
 DB 475 VLPATTIAENIRYGRDVTWDETEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGQKQ 534
 QY 541 RIAAALVRNPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADV 600
 DB 535 RIAAALVRNPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADV 594
 QY 601 IAGFDGVIIVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADSKSIDTLEMSSHD 660
 DB 595 IAGFDGVIIVEKGNHDELMKEGIYFKLVMTQAGNEIELENEVSKNEIDNLDMSKD 654
 QY 661 SSSLLIRKSTRSVRGSGQDRKLTKEALDESIPVPSFWRMKLNLTWPFYVGVPC 720
 DB 655 SASSLLIRKSTRSVRGSGQDRKLTKEALDESIPVPSFWRMKLNLTWPFYVGVPC 714
 QY 721 AIINGLOPAPAVIFSKIGITPNDDAETKQNSNLSLFLVLVLGIVSFITFLOGFTF 780
 DB 715 AIINGLOPAPAVIFSKIGITPNDDAETKQNSNLSLFLVLVLGIVSFITFLOGFTF 774
 QY 781 GKAGEILTRLRYMFRSMLRDQVSWFDDPKNTGALTTLRLANDAAQVKAIGASRLAIT 840
 DB 775 GKAGEILTRLRYMFRSMLRDQVSWFDDPKNTGALTTLRLANDAAQVKAIGATGARLAVIT 834
 QY 841 QNIANLGTGIIISLIYQWLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELEGAGKIA 900
 DB 835 QNIANLGTGIIISLIYQWLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELEGAGKIA 894
 QY 901 TEAIENFRVTSITOBKPEHMYDOSLOVPYNSLRKAHIFGITEFTQAMMYFSYAGCF 960
 DB 895 TEAIENFRVTSITOBKPEHMYDOSLOVPYNSLRKAHIFGITEFTQAMMYFSYAGCF 954
 QY 961 RFGAVILVHSLMSFEDVLVFSAVVFGAMAVGVSSFPADYAKAKVSAASHIIMIEKTP 1020
 DB 955 RFGAVILVHSLMSFEDVLVFSAVVFGAMAVGVSSFPADYAKAKVSAASHIIMIEKTP 1014
 QY 1021 IDSYSTGLKPNLTLEGNVFNVPYPTRLDIPVLQGLSLEVKKGQTLALVSSCGCKS 1080
 DB 1015 IDSYSTGLKPNLTLEGNVFNVPYPTRLDIPVLQGLSLEVKKGQTLALVSSCGCKS 1074
 QY 1081 TVVQLLERFYDPLAGKVLDDGKEIKQANVOMLAHLGIVSOEPIIFDCSISENIAYGDS 1140
 DB 1075 TVVQLLERFYDPMAGTVFLDGKEVQNLVQVLAHLGIVSOEPIIFDCSISENIAYGDS 1134
 QY 1141 RVVSOEEIVRAAKEANIHAIESLPNKYSTRVGDGKGTQLSGGQKORIAIARALVRQPHIL 1200
 DB 1135 RVVSOEEIVRAAKEANIHAIESLPNKYSTRVGDGKGTQLSGGQKORIAIARALVRQPHIL 1194
 QY 1201 LDEATSDALDTESEKVOEALDKAREGRTCVIAHRLSTIQNADLIVFQNGRVEHGH 1260
 DB 1195 LDEATSDALDTESEKVOEALDKAREGRTCVIAHRLSTIQNADLIVFQNGRVEHGH 1254
 QY 1261 QQLAOKGIYFSMVSVQAGAKR 1282
 DB 1255 QQLAOKGIYFSMVSVQAGAKR 1276

RESULT 3

A34786

multidrug resistance protein la - mouse
 C:Species: Mus musculus (house mouse)

C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C/Accession: A34786; A35671
R/Devault, A.; Gros, P.
Mol. Cell. Biol. 10, 1652-1663, 1990
A/Title: Two members of the mouse mdr gene family confer multidrug resistance with overl
A/Reference number: A34786; MUID: 90205845; PMID: 1969610
A/Accession: A34786
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1276 <DEV>
A/Cross-references: UNIPROT: P21447; UNIPARC: UPI0000028C58; GB: M30697; NID: G199111; PIDN:
R/Hsu, S.I.H.; Cohen, D.; Kirschner, L.S.; Lothstein, L.; Hartstein, M.; Horwitz, S.B.
Mol. Cell. Biol. 10, 3596-3606, 1990
A/Title: Structural analysis of the mouse mdr1a (P-glycoprotein) promoter reveals the ba
A/Reference number: A35671; MUID: 90287150; PMID: 1972547
A/Accession: A35671
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-525, 'HV', 528-938, 'S', 940-1035, 'V', 1037-1276 <HSU>
A/Cross-references: UNIPARC: UPI0000046660; GB: M33581; NID: G199104; PIDN: AAA39514.1; PID:
C/Suprafamily: multidrug resistance protein; ATP-binding cassette homology
C/Keywords: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; P-loop
F:406-600/Domain: ATP-binding cassette homology <ABC1>
F:423-431/Region: nucleotide-binding motif A (P-loop)
F:547-551/Region: nucleotide-binding motif B
F:1049-1245/Domain: ATP-binding cassette homology <ABC2>
F:1066-1074/Region: nucleotide-binding motif A (P-loop)
F:1192-1196/Region: nucleotide-binding motif B
F:429/Binding site: ATP (Lys) #status predicted
F:1072/Binding site: ATP (Lys) #status predicted

Query Match 88.1%; Score 5677.5; DB 2; Length 1276;
Best Local Similarity 87.1%; Pred. No. 1.2e-311; Indels 7; Gaps 2;
Matches 1116; Conservative 78; Mismatches 81;

QY 1 MDLEGRNGAEKKNFKNLNKSKDKKPKPTVSFSPRYSNWLDKLVVVGTLAAII 60
DB 1 MELEEDLKGRAD-KNFSKMGKSKKKEKPAVSVLTPRYAGWLDRLVNLVGTAAII 59
QY 61 HGAGLPFLMMLVFGDMTDTTANAGNLGDLGALLFNNTNSNITPTVPVNLDEDMTRYAY 120
DB 60 HGVALPFLMMLVFGDMTDSFASVGNVSK-----NSTNMSEADKRAFLEEMWTYAY 113
QY 121 YSGIGAGLVAAVIOVSFCLAGROHKIRKQPFHAIKROEIGVDVHDVGLNRLTD 180
DB 114 YTGIGAGLVIVAYIQVSFCLAGROHKIRKQPFHAIKROEIGVDVHDVGLNRLTD 173
QY 181 DYSKINEGIDKIGMFFQSMATPFTGIVGTGKWLTVILAIISPVLGLSAAVWAKILS 240
DB 174 DYSKINEGIDKIGMFFQSMATPFTGIVGTGKWLTVILAIISPVLGLSAGIWAIIIS 233
QY 241 SPTDKELAYAKAGAAVEELAAIRTVIAPGGOKKELRYNKNLEBAKRGIGIKKAITANI 300
DB 234 SPTDKELHAYAKAGAAVEELAAIRTVIAPGGOKKELRYNKNLEBAKRGIGIKKAITANI 293
QY 301 STGAAPFLIYASVALAFWTGTLVLKESVIGOVLFVFFSVLIGASVGOAPSIBAFAN 360
DB 294 SNGAAFLIYASVALAFWTGTLVLKESVIGOVLFVFFSVLIGASVGOAPSIBAFAN 353
QY 361 ARGAAFEIPKIIDNKPISIDYSKSHKPNKIKNLEFRNVHFSYPSRKEVILKGLNKKV 420
DB 354 ARGAAFEVFKIIDNKPISIDFSKSHKPNKIQNLEFKNIHFSYPSRKEVILKGLNKKV 413
QY 421 QSGQTVLVGNSGCGKSTTVQLMQLRYPDTEGMVSDGQDIRTINVRFLREIIGVVSQBP 480
DB 414 KSGQTVLVGNSGCGKSTTVQLMQLRYPDTEGMVSDGQDIRTINVRFLREIIGVVSQBP 473
QY 481 VLPATTIAENIRYGRDVTMDIEKAVKANAYDFIMKLPQKFDTLVGRGQAGLGGQKQ 540
DB 474 VLPATTIAENIRYGRDVTMDIEKAVKANAYDFIMKLPQKFDTLVGRGQAGLGGQKQ 533
QY 541 RTAIALRVNPKILLDLDEATSDALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 600

534 RTAIALRVNPKILLDLDEATSDALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 593
QY 601 IAGFDGIVIVEKGNHDELMKEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLESSH 660
DB 594 IAGFDGIVIVEKGNHDELMKEKGIYFKLVMTQTAGNEIELENADESKSEIDTLESSH 653
QY 661 SGSSLRKSTRRSRRSGSQQRKLTSTKALDESIPVSWRMKLNLTWEPYFVVGVPFC 720
DB 654 SGSSLRKSTRRSRRSGSQQRKLTSTKALDESIPVSWRMKLNLTWEPYFVVGVPFC 713
QY 721 AIINGLOPAPAVIFSKIGITFRNDDEAFKQNSLNFLSLFLVLGIVGIFITFFLQGGTF 780
DB 714 AIINGLOPAPAVIFSKIGITFRNDDEAFKQNSLNFLSLFLVLGIVGIFITFFLQGGTF 773
QY 781 GKAGBILTKRLRYMFRSMRLQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSLAIIIT 840
DB 774 GKAGBILTKRLRYMFRSMRLQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSLAIIIT 833
QY 841 QNIANLGTGIIISLYGQTLTLLLAIVPIAIAAGVEMKMLSGOALKDKKLEAGAKIA 900
DB 834 QNIANLGTGIIISLYGQTLTLLLAIVPIAIAAGVEMKMLSGOALKDKKLEAGAKIA 893
QY 901 TEAIENFRVSLTQEQKFEHMYDOSLOVPVYRNSLRKAHIFGITFTSQAMMYFVAGCF 960
DB 894 TEAIENFRVSLTQEQKFEHMYDOSLOVPVYRNSLRKAHIFGITFTSQAMMYFVAGCF 953
QY 961 RFGAYLVASHLMSFEDVLLVFSVAVFGAMAVGVQVSSFPADYAKAKVSAHIIIEKTPL 1020
DB 954 RFGAYLVASHLMSFEDVLLVFSVAVFGAMAVGVQVSSFPADYAKAKVSAHIIIEKTPL 1013
QY 1021 IDSYSTEGKNTLEGNTVFNENYTRLDIPVLQGLSLEVKGQTLALVSSGCGKKS 1080
DB 1014 IDSYSTEGKNTLEGNTVFNENYTRLDIPVLQGLSLEVKGQTLALVSSGCGKKS 1073
QY 1081 TVQQLLEFYDPLAGKVLLDGKEIKQLNVQWLRHGLVGVSOBPIIPDCSISENIAYGDS 1140
DB 1074 TVQQLLEFYDPLAGKVLLDGKEIKQLNVQWLRHGLVGVSOBPIIPDCSISENIAYGDS 1133
QY 1141 RVVSQEEIVRAAKEANIHAFTIESLPNKYSTRVGDKTQSGQKORIAIARALVRQPHIL 1200
DB 1134 RVVSQEEIVRAAKEANIHAFTIESLPNKYSTRVGDKTQSGQKORIAIARALVRQPHIL 1193
QY 1201 LDDEATSDALDTESEKVVQVQALDKARKGRTTIVIAHRLSTIONADLIVVFGVGRVKEHGT 1260
DB 1194 LDDEATSDALDTESEKVVQVQALDKARKGRTTIVIAHRLSTIONADLIVVFGVGRVKEHGT 1253
QY 1261 QQLLAQKGIYFSWVSQVQAGAKR 1282
DB 1254 QQLLAQKGIYFSWVSQVQAGAKR 1275

RESULT 4

DVM51

multidrug resistance protein 1 - mouse

N/Alternate names: P-glycoprotein 1

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C/Accession: A33719; A25057; I57510

R:Raymond, M.; Gros, P.

Proc. Natl. Acad. Sci. U.S.A. 86, 6488-6492, 1989

A/Title: Mammalian multidrug-resistance gene: correlation of exon organization with str

A/Reference number: A33719; MUID: 89367274; PMID: 2570420

A/Accession: A33719

A/Molecule type: DNA

A/Residues: 1-1276 <RAY>

A/Cross-references: UNIPROT: P06795; UNIPARC: UPI00000210D8

R:Gros, P.; Croop, J.; Housman, D.

Cell 47, 371-380, 1986

A/Title: Mammalian multidrug resistance gene: complete cDNA sequence indicates strong h

A/Reference number: A25057; MUID: 87028229; PMID: 3768958

A/Accession: A25057

A/Molecule type: mRNA

A/Residues: 1-1276 <GRO>

DB 61 HGAGLPLMGLVFGDMTTFANAGNLGDLGALLFNNNTSSNITDTVPVNNLEEDMTRYAY 120
QY 118 YSGIGAGLVAAAYIQVSWFCLAGROTHKIRKOPFFHAIMRQEQIGWFDVHDVGLNTRLTD 177
DB 121 YSGIGAGLVAAAYIQVSWFCLAGROTHKIRKOPFFHAIMRQEQIGWFDVHDVGLNTRLTD 180
QY 178 DVSKINEGIDGKIEMFPQSMATPTFTGIVGFTGKWLTLVILAIPLGSAVAWAKILS 237
DB 181 DVSKINEGIDGKIEMFPQSMATPTFTGIVGFTGKWLTLVILAIPLGSAVAWAKILS 240
QY 238 SPTDKELLAYAKAGAAVEEVLAAIRTVIAFGGOKKELERYNKLEAKRIGIKKALTANI 297
DB 241 SPTDKELLAYAKAGAAVEEVLAAIRTVIAFGGOKKELERYNKLEAKRIGIKKALTANI 300
QY 298 SIGAFLIIVASYALAFWYGTTLVLKSKYSIGQVLTFFSVLIGAFSVGQASPSIEAFAN 357
DB 301 SIGAFLIIVASYALAFWYGTTLVLKSKYSIGQVLTFFSVLIGAFSVGQASPSIEAFAN 360
QY 358 ARGAAPEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEPRNVHFSYPSKRVKILKGLNLKV 417
DB 361 ARGAAPEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEPRNVHFSYPSKRVKILKGLNLKV 420
QY 418 QSGQTVLAVGNSGCGSKSTTVQLMORLYDPTGEMVSDGQDIRTINVRFLREIIGVYSQEP 477
DB 421 QSGQTVLAVGNSGCGSKSTTVQLMORLYDPTGEMVSDGQDIRTINVRFLREIIGVYSQEP 480
QY 478 VLPATTIAENIRYGREVDVMEIEKAVEANAYDFIMKLPQKDTLVGERGAOLSGGQK 537
DB 481 VLPATTIAENIRYGREVDVMEIEKAVEANAYDFIMKLPQKDTLVGERGAOLSGGQK 540
QY 538 RIAIARALVNPXKILLDEATSAIDTSEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
DB 541 RIAIARALVNPXKILLDEATSAIDTSEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
QY 598 IAGFDGVIYVEKGNHDELMKEGIIYFKLVTMTAGNEIELENAADESKSIDTLEMSHD 657
DB 601 IAGFDGVIYVEKGNHDELMKEGIIYFKLVTMTAGNEIELENAADESKSIDTLEMSHD 660
QY 658 SGSSLRKSTRSVRGSGQDRKLTKEALDESIPVSWRIMKLNLTWPFVYGVVPC 717
DB 661 SGSSLRKSTRSVRGSGQDRKLTKEALDESIPVSWRIMKLNLTWPFVYGVVPC 720
QY 718 AINGGLQAPAFVIFSKIGIFTRNDAAETKRONSLFLLFLVLGIVSPITFPFLOGFTF 777
DB 721 AINGGLQAPAFVIFSKIGIFTRNDAAETKRONSLFLLFLVLGIVSPITFPFLOGFTF 780
QY 778 GKAGEILTKELRYVWFPSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAGLSRLAIT 837
DB 781 GKAGEILTKELRYVWFPSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAGLSRLAIT 840
QY 838 QNTANLGTGIIISLIYQWQLTLLLAIVPIIATAGVEMKLSQALDKKKELEGAKIA 897
DB 841 QNTANLGTGIIISLIYQWQLTLLLAIVPIIATAGVEMKLSQALDKKKELEGAKIA 900
QY 898 TEAIENFRVTSITQEQFHEMDQSLQVPRNSLRKAHIFGTFSTQAMTFYSYAGCF 957
DB 901 TEAIENFRVTSITQEQFHEMDQSLQVPRNSLRKAHIFGTFSTQAMTFYSYAGCF 960
QY 958 RFQAYILVAHSLMSEFEDVLLVFSVAVFGMAVGVSSPAPYAKAKVSAAHIMIEKTPIL 1017
DB 961 RFQAYILVAHSLMSEFEDVLLVFSVAVFGMAVGVSSPAPYAKAKVSAAHIMIEKTPIL 1020
QY 1018 IDSYSYEGKPNTEGNTVENVVNYPTPLDIPVLOGLSLEVKKGOTLALVSSGCGKS 1077
DB 1021 IDSYSYEGKPNTEGNTVENVVNYPTPLDIPVLOGLSLEVKKGOTLALVSSGCGKS 1080
QY 1078 TVVQLLERFYDPLAGKVLDDKEIKQLNVQWLAHGLGIVSQEPILFDCSISENIAYGDNS 1137
DB 1081 TVVQLLERFYDPLAGKVLDDKEIKQLNVQWLAHGLGIVSQEPILFDCSISENIAYGDNS 1140
QY 1138 RVVQSEIVRAAKVANTHAFIESLPNKYSTVGVGKGTQLSGGOKRIATARALVROPHIL 1197
DB 1197 RVVQSEIVRAAKVANTHAFIESLPNKYSTVGVGKGTQLSGGOKRIATARALVROPHIL 1200

QY 1198 LLDENTSALDTESEKVVQVSEALDKAREGRTCTIVIAHRLSTIQNADLIIVFQNGRVEKHGTH 1257
DB 1201 LLDENTSALDTESEKVVQVSEALDKAREGRTCTIVIAHRLSTIQNADLIIVFQNGRVEKHGTH 1260
QY 1258 QQLLAOKGIYFSMVSVQAGAKRQ 1280
DB 1261 QQLLAOKGIYFSMVSVQAGAKRQ 1283

RESULT 6

AAW44073
ID AAW44073 standard protein; 1280 AA.

AC AAW44073;

XX 25-MAR-2003 (revised)
DT 26-JUN-1998 (first entry)

XX Human multidrug resistance P-glycoprotein MDR1.

XX Human; multidrug resistance P-glycoprotein; MDR1; prokaryotic homologue.

XX Homo sapiens.

XX Key Location/Qualifiers
XX Region 1..640
FT /note= "MDR1-N from Fig 1"

FT Region 641..1280

FT /note= "MDR1-C from Fig 1"

XX WO9740160-A1.

XX 30-OCT-1997.

XX 24-APR-1997; 97WO-N000216.

XX 24-APR-1996; 96EP-00201094.

XX (UYGR-) RIJKSUNIV GRONINGEN.

XX Van Veen HW, Venema K, Bolhuis H, Konings WN;

XX WPI; 1997-535844/49.

XX Prokaryotic homologue of human multiple drug resistance protein - used to
screen for compounds that inhibit, or avoid, drug resistance.
Claim 10; Fig 1; 35pp; English.

The present invention describes a recombinant or isolated nucleic acid
(I), derived from a prokaryotic gene, which encodes at least a specific
and/or functional part of a transporter protein (Tp), or its derivatives,
which has functional and/or structural similarity with the P-glycoprotein
(PG) encoded by the human multidrug resistance (MDR) 1 gene. The present
sequence represents the human MDR1 protein, derived from MDR1-N and MDR1-
C as shown in the specification in figure 1. (I) is used to express
recombinant proteins; its fragments are also useful as probes and primers
for detection and amplification of related DNA. The protein produced, or
cells expressing them, are used to determine if substances can inhibit,
or avoid, MDR proteins, and in a screening method for identifying
compounds that inhibit transport of cytotoxic substances from cells.
Also, cells with a transmembrane protein, especially where expressed from
C (I), can provide (additional) MDR, particularly for use as a model system
to study mechanisms of action of PG. (Updated on 25-MAR-2003 to correct
PF field.)

XX Sequence 1280 AA;

Query Match 96.8%; Score 6218; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1237; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDLEGRNGGAEKQNF FKLNNKS KDKCKKPTVSVFSMPRYSNMLDKLYMVVGTAAII 60
 Db 1 MDLEGRNGGAKKQNF FKLNNKSEKDKCKKPTVSVFSMPRYSNMLDKLYMVVGTAAII 60
 QY 61 HGAGLPLMKLVFGDMTDTFANAGNLGDLGALLTNSNITDTPVNVNLEDMDTRYAYTSG 120
 Db 61 HGAGLPLMKLVFGDMTDTFANAGNLGDLGALLTNSNITDTPVNVNLEDMDTRYAYTSG 120
 QY 121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKQFFPHAIMRQEIQWDFVHDVDELNTRLTDDVS 180
 Db 121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKQFFPHAIMRQEIQWDFVHDVDELNTRLTDDVS 180
 QY 181 KINEGIGDKIMFPMOSMAFTFTGIVGFTFRGWKLTLVILAIISPVGLSAAVWAKILSFT 240
 Db 181 KINEGIGDKIMFPMOSMAFTFTGIVGFTFRGWKLTLVILAIISPVGLSAAVWAKILSFT 240
 QY 241 DKELLAYAKAGAVAEVLAAITVIAFGGKKLELYNKNLEAKRIGIKKAITANISIG 300
 Db 241 DKELLAYAKAGAVAEVLAAITVIAFGGKKLELYNKNLEAKRIGIKKAITANISIG 300
 QY 301 AAFELIYASALAFWYGTTLVLSEYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 360
 Db 301 AAFELIYASALAFWYGTTLVLSEYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 360
 QY 361 AAFELIYASALAFWYGTTLVLSEYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 420
 Db 361 AAFELIYASALAFWYGTTLVLSEYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 420
 QY 421 QTVLVGNSGCKSTTVQMLQRYDPTGWSVDGDIINVRFLREIIGVVSQEPVLF 480
 Db 421 QTVLVGNSGCKSTTVQMLQRYDPTGWSVDGDIINVRFLREIIGVVSQEPVLF 480
 QY 481 ATTIAENTRYGREDVTMDIEKAVKEANAYDFTMKLPQKFTLVGERGAQLSGGQKORIA 540
 Db 481 ATTIAENTRYGREDVTMDIEKAVKEANAYDFTMKLPQKFTLVGERGAQLSGGQKORIA 540
 QY 541 ZARALVRNPKILLDEATSEALDTESEAVVOVALDKARKORTTIVIAHRLSTVRNADVIAG 600
 Db 541 ZARALVRNPKILLDEATSEALDTESEAVVOVALDKARKORTTIVIAHRLSTVRNADVIAG 600
 QY 601 PDGVTIVEKGNDELKMKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSHDSGS 660
 Db 601 PDGVTIVEKGNDELKMKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSHDSGS 660
 QY 661 SLIRKSTRSVRSGQDRKLSKEALDESIPVSVFWRIMKMLNLTWPYFVGVVFCAL 720
 Db 661 SLIRKSTRSVRSGQDRKLSKEALDESIPVSVFWRIMKMLNLTWPYFVGVVFCAL 720
 QY 721 NGGLQAPAFVFSKIIGIFTRNDDEATKRONSLFSLLLFLVLGIVSFIFPFGQFTFGKA 780
 Db 721 NGGLQAPAFVFSKIIGIFTRNDDEATKRONSLFSLLLFLVLGIVSFIFPFGQFTFGKA 780
 QY 781 GELTLKRLRVWFRSMLRQDVSWDFDPKNTTGALTTRLANDAAQVKGALSRLLAITONI 840
 Db 781 GELTLKRLRVWFRSMLRQDVSWDFDPKNTTGALTTRLANDAAQVKGALSRLLAITONI 840
 QY 841 ANLGTGIIISLIYCWOLTLALLAIVPIIAIAGVVMKLSGQALKDKELEGAGKIATEA 900
 Db 841 ANLGTGIIISLIYCWOLTLALLAIVPIIAIAGVVMKLSGQALKDKELEGAGKIATEA 900
 QY 901 IENFRVTVLSQOKFHEMTDQSLQVYRNSLRKAHIFGTFTQMTQWYFVAGCFREG 960
 Db 901 IENFRVTVLSQOKFHEMTDQSLQVYRNSLRKAHIFGTFTQMTQWYFVAGCFREG 960
 QY 961 AYLVASHLSMFEDVLLVFSVAFGMAVGVQSVFADYAKVSAHIMIIEKTPILDS 1020
 Db 961 AYLVASHLSMFEDVLLVFSVAFGMAVGVQSVFADYAKVSAHIMIIEKTPILDS 1020
 QY 1021 YSTEGLKPNLTLEGNTVNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSGSGCKSTTV 1080
 Db 1021 YSTEGLKPNLTLEGNTVNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSGSGCKSTTV 1080
 QY 1081 QLLERFYDPLAGKVLDDGKEIKQLNVQWLAHGLIVSQEPIILPDCSISENIAYGDSNRV 1140

Db 1081 QLLERFYDPLAGKVLDDGKEIKQLNVQWLAHGLIVSQEPIILPDCSISENIAYGDSNRV 1140
 QY 1141 SQEEIVRAAKEANIHAIESLPNPKYSTRVGDKGTQLSGGQKORIAIARALVRQPHILLD 1200
 Db 1141 SQEEIVRAAKEANIHAIESLPNPKYSTRVGDKGTQLSGGQKORIAIARALVRQPHILLD 1200
 QY 1201 EATSALDTESEKVOEALDKARSGRTCTIVIAHRLSTLSTIONADLIVVFONGRVKHEGTHQOL 1260
 Db 1201 EATSALDTESEKVOEALDKARSGRTCTIVIAHRLSTLSTIONADLIVVFONGRVKHEGTHQOL 1260
 QY 1261 LAQKGIYFSMVSVQAGAKRQ 1280
 Db 1261 LAQKGIYFSMVSVQAGAKRQ 1280

RESULT 7
 AAY58186
 ID AAY58186 standard; protein; 1280 AA.
 XX
 AC AAY58186;
 DT 14-MAR-2000 (first entry)
 XX
 DE Human wild-type multidrug resistance-1 (MDR-1) protein.
 XX
 KW Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
 KW haematopoietic stem cell; transduction; bone marrow transplantation;
 KW chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
 KW genetic defect; thalassaemia; Gauchier's disease; sickle cell anaemia;
 KW leukaemia; ex vivo expansion; cytokine; wild-type.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Misc-difference 185
 XX
 FT Note="This residue is Val in a mutant MDR-1 (AAY58187)".
 XX
 FN WO9961589-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 27-MAY-1999; 99WO-US011825.
 XX
 PR 28-MAY-1998; 98US-0086988P.
 XX
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX
 PI Sorrentino B, Bunting K;
 XX
 XX WPI; 2000-072615/06.
 DR N-PSDB; AAZ49332.
 XX
 PT Ex vivo expansion of hematopoietic stem cells transduced with a sequence
 PT encoding human multidrug resistance-1, used for bone marrow
 PT transplantation.
 XX
 PS Claim 10; Page 71-79; 113pp; English.
 XX
 CC This sequence represents human wild-type multidrug resistance protein MDR
 CC -1. MDR-1 is a transmembrane efflux pump, responsible for the export of
 CC drugs from certain cells, particularly cancer cells. Wild-type MDR-1
 CC shows increased resistance to etoposide and decreased resistance to vinca
 CC alkaloids compared with a mutant form (AAY58187) where the Gly at
 CC position 185 is replaced by Val. The invention relates to transducing
 CC haematopoietic stem cells with nucleic acid encoding an MDR protein and
 CC culturing the modified cells. The modified haematopoietic stem cells are
 CC useful in bone marrow transplantation (to reconstitute haematopoietic
 CC systems in patients who have undergone chemotherapy or radiation therapy)
 CC and in ex vivo gene therapy of genetic defects in cells derived from
 CC haematopoietic stem cells, e.g., thalassaemia, Gauchier's disease, sickle
 CC cell anaemia or leukaemia. The modified cells can also be used to
 CC identify factors involved in regulating proliferation and differentiation

Query Match 96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEGKNNFKLNKSKDKCKRKPTVSFVSFMYRNWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGAEGKNNFKLNKSKDKCKRKPTVSFVSFMYRNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTTPANAGNLGDLGALLTNSNITDTPVPMLEEDMTYATYISG 120
DB 61 HGAGLPLMLVFGDMTTPANAGNLGDLGALLTNSNITDTPVPMLEEDMTYATYISG 120
QY 121 IGAGLVAAVYQVSFWCLAAAGROHKKRQFHAIMRQEIQWDFVHDVDELNRLTDDVS 180
DB 121 IGAGLVAAVYQVSFWCLAAAGROHKKRQFHAIMRQEIQWDFVHDVDELNRLTDDVS 180
QY 181 KINEGIGDKIGMFFQSMATPFTGTFVGTGKWLTLVLAISPVGLSAAVWAKILSSFT 240
DB 181 KINEGIGDKIGMFFQSMATPFTGTFVGTGKWLTLVLAISPVGLSAAVWAKILSSFT 240
QY 241 DXELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG 300
DB 241 DXELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG 300
QY 301 APELLIYASVALAFWYGTTLVLSEYISGOVLTVFVSRLIGAFSVGOASPIEAFANARG 360
DB 301 APELLIYASVALAFWYGTTLVLSEYISGOVLTVFVSRLIGAFSVGOASPIEAFANARG 360
QY 361 AAFBIFKIIDNKPISIDSYSGHKKPDNKNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
DB 361 AAFBIFKIIDNKPISIDSYSGHKKPDNKNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
QY 421 QTVLVNCSGCKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVWSQEPVLF 480
DB 421 QTVLVNCSGCKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVWSQEPVLF 480
QY 481 ATTAEINIRGRENVTWDETEKAVEANAYDFIMKLPKPDTLVGERGAOLSGQOKORIA 540
DB 481 ATTAEINIRGRENVTWDETEKAVEANAYDFIMKLPKPDTLVGERGAOLSGQOKORIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIIVEKGNHDELMEKEGIYFKLVMTQAGNEVELENAADESKSIDALESSNDSRS 660
DB 601 FDDGVIIVEKGNHDELMEKEGIYFKLVMTQAGNEVELENAADESKSIDALESSNDSRS 660
QY 661 SLIRKSTRSRVSGSQDRKLSKEALDESIIPVSWFWRIMKLNLTWPYFVGVVFCALI 720
DB 661 SLIRKSTRSRVSGSQDRKLSKEALDESIIPVSWFWRIMKLNLTWPYFVGVVFCALI 720
QY 721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLVLGIVSFITPFLQFTFGKA 780
DB 721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLVLGIVSFITPFLQFTFGKA 780
QY 781 GEILTKELRVYFVSMRLQDVSWDFDPKNTTGAITRLANDAAQVKGAGISRLAITONI 840
DB 781 GEILTKELRVYFVSMRLQDVSWDFDPKNTTGAITRLANDAAQVKGAGISRLAITONI 840
QY 841 ANLGTGIIISLIGWQLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA 900
DB 841 ANLGTGIIISLIGWQLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA 900
QY 901 IENPRTVVSLSLTOEQKEFHYDQSLQVPRNSLRKAHIFGTFSTQAMMYFSYACGRFPG 960
DB 901 IENPRTVVSLSLTOEQKEFHYDQSLQVPRNSLRKAHIFGTFSTQAMMYFSYACGRFPG 960
QY 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIIIMIEKTLPLIDS 1020
DB 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIIIMIEKTLPLIDS 1020
QY 1021 YSTGLKPNLTLEGNVTNEVFNPTRLDIPVLQGLSLEVKKGQTLALVGSOGCKSTTV 1080

DB 1021 YSTGLKPNLTLEGNVTNEVFNPTRLDIPVLQGLSLEVKKGQTLALVGSOGCKSTTV 1080
QY 1081 QLLERFPYDLACKVLLDGKEIKQINQWOLRAHLGTVSOEPIILFDCSISENIAYGDSRVV 1140
DB 1081 QLLERFPYDLACKVLLDGKEIKQINQWOLRAHLGTVSOEPIILFDCSISENIAYGDSRVV 1140
QY 1141 SOEETVRAAKENIAHAFIESLPNKYSTYRVDGKGTOLSGQOKORIAIARALVRPHILLD 1200
DB 1141 SOEETVRAAKENIAHAFIESLPNKYSTYRVDGKGTOLSGQOKORIAIARALVRPHILLD 1200
QY 1201 EATSALDTESEKVOEALDKAREGTCIVIAHRLSTIONADLIVVFGNGRVEKHEGTHOOL 1260
DB 1201 EATSALDTESEKVOEALDKAREGTCIVIAHRLSTIONADLIVVFGNGRVEKHEGTHOOL 1260
QY 1261 LAQGIYFSMVSVOAGAKRQ 1280
DB 1261 LAQGIYFSMVSVOAGAKRQ 1280

RESULT 11
US-09-817-762-3
Sequence 3, Application US/09817762
Patent No. 6886774

GENERAL INFORMATION:
APPLICANT: Spalding, Edgar P.
APPLICANT: No. 6858774, Bosl
TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
TITLE OF INVENTION: Plants
FILE REFERENCE: 13238-00061
CURRENT APPLICATION NUMBER: US/09/817,762
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: PCT/US99/22363
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,814
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank P08183
DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match 96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEGKNNFKLNKSKDKCKRKPTVSFVSFMYRNWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGAEGKNNFKLNKSKDKCKRKPTVSFVSFMYRNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTTPANAGNLGDLGALLTNSNITDTPVPMLEEDMTYATYISG 120
DB 61 HGAGLPLMLVFGDMTTPANAGNLGDLGALLTNSNITDTPVPMLEEDMTYATYISG 120
QY 121 IGAGLVAAVYQVSFWCLAAAGROHKKRQFHAIMRQEIQWDFVHDVDELNRLTDDVS 180
DB 121 IGAGLVAAVYQVSFWCLAAAGROHKKRQFHAIMRQEIQWDFVHDVDELNRLTDDVS 180
QY 181 KINEGIGDKIGMFFQSMATPFTGTFVGTGKWLTLVLAISPVGLSAAVWAKILSSFT 240
DB 181 KINEGIGDKIGMFFQSMATPFTGTFVGTGKWLTLVLAISPVGLSAAVWAKILSSFT 240
QY 241 DXELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG 300
DB 241 DXELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG 300
QY 301 APELLIYASVALAFWYGTTLVLSEYISGOVLTVFVSRLIGAFSVGOASPIEAFANARG 360
DB 301 APELLIYASVALAFWYGTTLVLSEYISGOVLTVFVSRLIGAFSVGOASPIEAFANARG 360
QY 361 AAFBIFKIIDNKPISIDSYSGHKKPDNKNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
DB 361 AAFBIFKIIDNKPISIDSYSGHKKPDNKNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
QY 421 QTVLVNCSGCKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVWSQEPVLF 480
DB 421 QTVLVNCSGCKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVWSQEPVLF 480
QY 481 ATTAEINIRGRENVTWDETEKAVEANAYDFIMKLPKPDTLVGERGAOLSGQOKORIA 540
DB 481 ATTAEINIRGRENVTWDETEKAVEANAYDFIMKLPKPDTLVGERGAOLSGQOKORIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIIVEKGNHDELMEKEGIYFKLVMTQAGNEVELENAADESKSIDALESSNDSRS 660
DB 601 FDDGVIIVEKGNHDELMEKEGIYFKLVMTQAGNEVELENAADESKSIDALESSNDSRS 660
QY 661 SLIRKSTRSRVSGSQDRKLSKEALDESIIPVSWFWRIMKLNLTWPYFVGVVFCALI 720
DB 661 SLIRKSTRSRVSGSQDRKLSKEALDESIIPVSWFWRIMKLNLTWPYFVGVVFCALI 720
QY 721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLVLGIVSFITPFLQFTFGKA 780
DB 721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLVLGIVSFITPFLQFTFGKA 780
QY 781 GEILTKELRVYFVSMRLQDVSWDFDPKNTTGAITRLANDAAQVKGAGISRLAITONI 840
DB 781 GEILTKELRVYFVSMRLQDVSWDFDPKNTTGAITRLANDAAQVKGAGISRLAITONI 840
QY 841 ANLGTGIIISLIGWQLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA 900
DB 841 ANLGTGIIISLIGWQLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA 900
QY 901 IENPRTVVSLSLTOEQKEFHYDQSLQVPRNSLRKAHIFGTFSTQAMMYFSYACGRFPG 960
DB 901 IENPRTVVSLSLTOEQKEFHYDQSLQVPRNSLRKAHIFGTFSTQAMMYFSYACGRFPG 960
QY 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIIIMIEKTLPLIDS 1020
DB 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIIIMIEKTLPLIDS 1020
QY 1021 YSTGLKPNLTLEGNVTNEVFNPTRLDIPVLQGLSLEVKKGQTLALVGSOGCKSTTV 1080

301 AAFLLIYASALAFWYGTTLVLGSEYSGOVLTVFSSVLIGAPSVGQASPSIEAFANARG 360
 361 AAFIFIKIDNKPSIDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420
 361 AAYEIFIKIDNKPSIDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420
 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
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 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQKORIA 540
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 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
 601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 661 SLIRKSTRSVRGSGQDRLKSTKEALDESIIPVSWFWRIMKLNLTWFPYVGVFCALI 720
 661 SLIRKSTRSVRGSGQDRLKSTKEALDESIIPVSWFWRIMKLNLTWFPYVGVFCALI 720
 721 NGGLQPAFAVIFSKIIGFTNDDAETKRONSNLFSLLFLVLGIVSPITTFPLOGFTFGKA 780
 721 NGGLQPAFAVIFSKIIGFTNDDAETKRONSNLFSLLFLVLGIVSPITTFPLOGFTFGKA 780
 781 GEILTKLRVNVFMSRLQDVSFDDPKNTTGALTTRLANDAAQVKGAGISRLAITONI 840
 781 GEILTKLRVNVFMSRLQDVSFDDPKNTTGALTTRLANDAAQVKGAGISRLAITONI 840
 841 ANLGTGIIISLYGWLTLALLAIVPIIAIAGVEMKMLSGOALKKKELEGACKIATEA 900
 841 ANLGTGIIISLYGWLTLALLAIVPIIAIAGVEMKMLSGOALKKKELEGACKIATEA 900
 901 IENFTVVSLLTQEQFHEMYDQSLQVYPYNSIRKRAHIFGTFSPFTQAMVYSYAGCPRFG 960
 901 IENFTVVSLLTQEQFHEMYDQSLQVYPYNSIRKRAHIFGTFSPFTQAMVYSYAGCPRFG 960
 961 AYLVAHMSFEDVLLVPSAVVFGAMAVGQVSSFAPDYAKAVSAAHIMIEKTPLIDS 1020
 961 AYLVAHMSFEDVLLVPSAVVFGAMAVGQVSSFAPDYAKAVSAAHIMIEKTPLIDS 1020
 1021 YSTEGLKENTLEGNVTNEVVPNTPLDIPVLOGLSLEVKKGOTLALVSGSGCGKSTVV 1080
 1021 YSTEGLKENTLEGNVTNEVVPNTPLDIPVLOGLSLEVKKGOTLALVSGSGCGKSTVV 1080
 1081 QLLERFYDPLAGKVLDDGKEIKQLNVOLRAHLGIVSQEPILFDCSISENIAYGDSRVV 1140
 1081 QLLERFYDPLAGKVLDDGKEIKQLNVOLRAHLGIVSQEPILFDCSISENIAYGDSRVV 1140
 1141 SQEIVRAAKANTHAFTESIPNKYSTVKGDKTQSGGQKORIAIARALVRPHILLD 1200
 1141 SQEIVRAAKANTHAFTESIPNKYSTVKGDKTQSGGQKORIAIARALVRPHILLD 1200
 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIONADLIIVVFQNGRVEKHGTHOOL 1260
 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIONADLIIVVFQNGRVEKHGTHOOL 1260
 1261 LAQGIYFSMVSVQAGAKRQ 1280
 1261 LAQGIYFSMVSVQAGAKRQ 1280

RESULT 12

US-09-584-586-4
 ; Sequence 4, Application US/09584586
 ; Patent No: 693150
 ; GENERAL INFORMATION:
 ; APPLICANT: Sorrentino, Brian

APPLICANT: Bunting, Kevin
 TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 FILE REFERENCE: MDR-1 METHODS OF USE THEREOF
 CURRENT APPLICATION NUMBER: US/09/584,586
 CURRENT FILING DATE: 2000-05-31
 EARLIER APPLICATION NUMBER: US 60/086,988
 EARLIER FILING DATE: 1998-05-28
 EARLIER APPLICATION NUMBER: PCT/US99/11825
 EARLIER FILING DATE: 1999-05-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patent in Ver. 2.0
 SEQ ID NO 4
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Human MDR 185-V
 US-09-584-586-4

Query Match 96.6%; Score 6209; DB 2; Length 1280;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGDRNGAEGKGNPFKLNKSKKKKKKPTVSFMSFRYSNWLDKLYMVVGTLLAAII 60
 Db 1 MDLEGDRNGAEGKGNPFKLNKSKKKKKKPTVSFMSFRYSNWLDKLYMVVGTLLAAII 60
 Qy 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNMLEEDTRYAYYSG 120
 Db 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNMLEEDTRYAYYSG 120
 Qy 121 IGAGLVAAIYQVSPFCLAAAGROHKKQPHAIHQISGHPDHDVDELNRLTDDYS 180
 Db 121 IGAGLVAAIYQVSPFCLAAAGROHKKQPHAIHQISGHPDHDVDELNRLTDDYS 180
 Qy 181 KINEGIDKIMGFQSMATFTFTGIVGFTGKWLTLVILAIAPVLGLSAVWAKILSSFT 240
 Db 181 KINEGIDKIMGFQSMATFTFTGIVGFTGKWLTLVILAIAPVLGLSAVWAKILSSFT 240
 Qy 241 DKELLAYAKAGAAVEVLAAIITVIAFGGOKKELERYNKNLEAKRIGIKAITANISIG 300
 Db 241 DKELLAYAKAGAAVEVLAAIITVIAFGGOKKELERYNKNLEAKRIGIKAITANISIG 300
 Qy 301 AAFLLIYASALAFWYGTTLVLGSEYSGOVLTVFSSVLIGAPSVGQASPSIEAFANARG 360
 Db 301 AAFLLIYASALAFWYGTTLVLGSEYSGOVLTVFSSVLIGAPSVGQASPSIEAFANARG 360
 Qy 361 AAFIPIKIDNKPSIDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420
 Db 361 AAFIPIKIDNKPSIDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420
 Qy 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
 Db 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
 Qy 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQKORIA 540
 Db 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQKORIA 540
 Qy 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
 Db 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
 Qy 601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 Db 601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 Qy 661 SLIRKSTRSVRGSGQDRLKSTKEALDESIIPVSWFWRIMKLNLTWFPYVGVFCALI 720
 Db 661 SLIRKSTRSVRGSGQDRLKSTKEALDESIIPVSWFWRIMKLNLTWFPYVGVFCALI 720
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Db 721 NGGLQAPAFIISKIIGVTRIDDPETKRONSLFSLFLALGIISFTFFLQGTFGKA 780
Qy 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGALTRLANDAAQVKGAGISRLAIITONI 840
Db 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGALTRLANDAAQVKGAGISRLAVITONI 840
Qy 841 ANLGTGIIISLYGWLTLIIAIVPIIAAGVEMKMLSGOALKDKKELEGAGKATEA 900
Db 841 ANLGTGIIISLYGWLTLIIAIVPIIAAGVEMKMLSGOALKDKKELEGAGKATEA 900
Qy 901 IENERTVVSLSQEQFEMHYDQSLQVPRNSLRKAHIGITFSTQAMWFSYACGCRFG 960
Db 901 IENERTVVSLSQEQFEMHYDQSLQVPRNSLRKAHIGITFSTQAMWFSYACGCRFG 960
Qy 961 AYLVHSLMSPEDVLLVFSVAVFGAMAVQVSSPAPDYAKAKVSAHIIIEKTPILDS 1020
Db 961 AYLVHSLMSPEDVLLVFSVAVFGAMAVQVSSPAPDYAKAKVSAHIIIEKTPILDS 1020
Qy 1021 YSTEGLKPNTEGNTVEVFNYPTRIDIPVLQGLSLEVKKGOTLALVSSGCGKSTVV 1080
Db 1021 YSTEGLKPNTEGNTVEVFNYPTRIDIPVLQGLSLEVKKGOTLALVSSGCGKSTVV 1080
Qy 1081 QLLERFVDPPLAGKVLIDGKEIKOLNVOWLRAHLGIVSOEPLPDCSISENIAYGDSRVV 1140
Db 1081 QLLERFVDPPLAGKVLIDGKEIKOLNVOWLRAHLGIVSOEPLPDCSISENIAYGDSRVV 1140
Qy 1141 SOBEIVRAAKANIHAFFIESLPNKYSTVGDKGTQSGGQKQRIATARALVRQPHILLD 1200
Db 1141 SOBEIVRAAKANIHAFFIESLPNKYSTVGDKGTQSGGQKQRIATARALVRQPHILLD 1200
Qy 1201 EATSALDTESEKVOBALDKAREGRICIVIAHRLSTIONADLIIVFQNGRVEKHGTHOOL 1260
Db 1201 EATSALDTESEKVOBALDKAREGRICIVIAHRLSTIONADLIIVFQNGRVEKHGTHOOL 1260
Qy 1261 LAQGIYFMSVSVQAGAKRQ 1280
Db 1261 LAQGIYFMSVSVQAGAKRQ 1280

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RESULT 13
US-08-583-276-19
; Sequence 19, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Carella, Byrne, Bain, Gilfillan,
; ADDRESS: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712

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; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; US-08-583-276-19

Query Match 96.6%; Score 6206; DB 1; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGRNGAGKKNPFKLNKSKDKKPKPTVSFPMFYSNWLKLYMVVGTLLAAII 60
Db 1 MDLEGRNGAGKKNPFKLNKSKDKKPKPTVSFPMFYSNWLKLYMVVGTLLAAII 60
Qy 61 HGAGLPMLLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPMNLEBDMTRYAYYSG 120
Db 61 HGAGLPMLLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPMNLEBDMTRYAYYSG 120
Qy 121 IGAGVLVAAYIQVSPFWCLAAAGRIHKIRKQFPHAIMRQEIHFVDFVHVGELNLTDDVS 180
Db 121 IGAGVLVAAYIQVSPFWCLAAAGRIHKIRKQFPHAIMRQEIHFVDFVHVGELNLTDDVS 180
Qy 181 KINEGIGDKIGMPFOSMATFFTFGIVGTGTRGKLTVLILAISPVLGLSAAVWAKILSST 240
Db 181 KINEGIGDKIGMPFOSMATFFTFGIVGTGTRGKLTVLILAISPVLGLSAAVWAKILSST 240
Qy 241 DKELLAYAKAGAVAEVLAAITRTVAFGGQKKELEKRYNKNLEAKRIGIKKAITANISIG 300
Db 241 DKELLAYAKAGAVAEVLAAITRTVAFGGQKKELEKRYNKNLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASALAFWYGTTLVLSKEYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Db 301 AAFLLIYASALAFWYGTTLVLSKEYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Qy 361 AAFEFKIIDNKPSIDSYSGKHGPDNFKGNLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
Db 361 AAFEFKIIDNKPSIDSYSGKHGPDNFKGNLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
Qy 421 QTVLVGNSGCGKSTTVQLMQRLYDPTBEGMVSVDQDITRTINVRFLREIIGVVSQEPVLF 480
Db 421 QTVLVGNSGCGKSTTVQLMQRLYDPTBEGMVSVDQDITRTINVRFLREIIGVVSQEPVLF 480
Qy 481 ATTIAENIRYGRVDVWDEIEKAVKEANAYDFIMKLPOKEDTLVGERGAQLSGGQKORIA 540
Db 481 ATTIAENIRYGRVDVWDEIEKAVKEANAYDFIMKLPOKEDTLVGERGAQLSGGQKORIA 540
Qy 541 IARALVRNPKILLDEATSEAVVQVALDKARKGRITIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSEAVVQVALDKARKGRITIVIAHRLSTVRNADVIAG 600
Qy 601 PDDGVIVKGNHDELMKEKGIYFKLVTMQTAGNEIELENAADESKSIDLEMSHDSGS 660
Db 601 PDDGVIVKGNHDELMKEKGIYFKLVTMQTAGNEIELENAADESKSIDLEMSHDSGS 660
Qy 661 SLIKRSTRSVRSGSQDRLSTKEALDSIPVSWFRIMKLNLTWPYFVGVFCAII 720
Db 661 SLIKRSTRSVRSGSQDRLSTKEALDSIPVSWFRIMKLNLTWPYFVGVFCAII 720
Qy 721 NGGLQAPAFIISKIIGVTRIDDPETKRONSLFSLFLALGIISFTFFLQGTFGKA 780
Db 721 NGGLQAPAFIISKIIGVTRIDDPETKRONSLFSLFLALGIISFTFFLQGTFGKA 780
Qy 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGALTRLANDAAQVKGAGISRLAIITONI 840
Db 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGALTRLANDAAQVKGAGISRLAVITONI 840
Qy 841 ANLGTGIIISLYGWLTLIIAIVPIIAAGVEMKMLSGOALKDKKELEGAGKATEA 900

```

Db 841 ANLGTGIIISPIYCHQTLTLLLAIVPIIATAGVVMKLSQALXDKKELEGAGKIATEA 900
Qy 901 IENFRTVSVLTQEQKFEHMYDOSLOVPYRNSLRKAHIFGIIIFTSFTQAMMYSYAGCPRFG 960
Db 901 IENFRTVSVLTQEQKFEHMYAQSLOVPYRNSLRKAHIFGIIIFTSFTQAMMYSYAGCPRFG 960
Qy 961 AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIIEKTPILDS 1020
Db 961 AYLVAHKLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAAHIMIIIEKTPILDS 1020
Qy 1021 YSTGLKPNLTLEGNTVFNVEVFNYPTRDIPVLQGLSLFVKGGQTALVGSOGCKSTV 1080
Db 1021 YSTGLKPNLTLEGNTVFNVEVFNYPTRDIPVLQGLSLFVKGGQTALVGSOGCKSTV 1080
Qy 1081 QLLERFYDPLAGVLLDQKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENTAYGDSNRV 1140
Db 1081 QLLERFYDPLAGVLLDQKEIKRLNVQWMLRAHLGIVSQEPILFDCSIAENTAYGDSNRV 1140
Qy 1141 SOEETVRAAKEANIHAFTESLPNKYSTRVGDKGTQSGQKQRIARALVRQPHILLD 1200
Db 1141 SOEETVRAAKEANIHAFTESLPNKYSTRVGDKGTQSGQKQRIARALVRQPHILLD 1200
Qy 1201 EATSALDTESEKVVQEQALDKAREGTCIVIAHRLSTIQNADLIVVFQNGRVEKHTHOOL 1260
Db 1201 EATSALDTESEKVVQEQALDKAREGTCIVIAHRLSTIQNADLIVVFQNGRVEKHTHOOL 1260
Qy 1261 LAQKGIYFSMVSQAGAKRQ 1280
Db 1261 LAQKGIYFSMVSQAGTKRQ 1280

RESULT 14
5206352-4
; Patent No. 5206352
; APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
; Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO: 4:
; LENGTH: 1280

Query Match 96.6%; Score 6206; DB 7; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;
Qy 1 MDLEGRNGAGKONFFKLNKSKDKKPKPTVSVFSMFRYSNWLKLYVMVGTLLAII 60
Db 1 MDLEGRNGAGKONFFKLNKSKDKKPKPTVSVFSMFRYSNWLKLYVMVGTLLAII 60
Qy 61 HGAGLPLMMLVFQDMTDTTANAGNLGDLGALLTNSNITDTPVPMNLEDMTRYIYYS 120
Db 61 HGAGLPLMMLVFQDMTDTTANAGNLGDLGALLTNSNITDTPVPMNLEDMTRYIYYS 120
Qy 121 IGAGVLVAAYIQVSFWCLAGRQIHKIQKQFHAIIMRQIENWDFVHVGELNTRLTDDVS 180
Db 121 IGAGVLVAAYIQVSFWCLAGRQIHKIQKQFHAIIMRQIENWDFVHVGELNTRLTDDVS 180
Qy 181 KINQEGIDKIGMFFQSMATFFFTGFIVGFTGRGWLTLVLAISPVLGLSAVWAKILSSFT 240
Db 181 KINQVIGDKIGMFFQSMATFFFTGFIVGFTGRGWLTLVLAISPVLGLSAVWAKILSSFT 240
Qy 241 DKELLAYAKAGVAEVLAAIRTVIAFGQKKLEBRYNNKLEAKRIGIKKAITANISIG 300

Db 241 DKELLAYAKAGVAEVLAAIRTVIAFGQKKLEBRYNNKLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASVALAFWYGTTLVLVSKEYSIGQVLTFFSVLIGAFSVGOASPSIEAFANARG 360
Db 301 AAFLLIYASVALAFWYGTTLVLVSKEYSIGQVLTFFSVLIGAFSVGOASPSIEAFANARG 360
Qy 361 AAFEIFKIIDNKPSIDSYSKSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420
Db 361 AAFEIFKIIDNKPSIDSYSKSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420
Qy 421 QTVLVCNSCGKSTTVLMQRLYDPTGEMVSDGDIRTINVRFLREIIGVVSQEPVLF 480
Db 421 QTVLVCNSCGKSTTVLMQRLYDPTGEMVSDGDIRTINVRFLREIIGVVSQEPVLF 480
Qy 481 ATTIAENIRYGRBVTMDIEKAVKEANAYDFIMKLPQKPDITLVGERCAOLSGQKORIA 540
Db 481 ATTIAENIRYGRBVTMDIEKAVKEANAYDFIMKLPQKPDITLVGERCAOLSGQKORIA 540
Qy 541 IARALVRNPKILLDEATSDALDTESEAVVOALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSDALDTESEAVVOALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Qy 601 FDDGVIVKGNHDELMKEKGIYFKLVTMQTAGNEIELENAADESKSEIDTLEMSSHDSGS 660
Db 601 FDDGVIVKGNHDELMKEKGIYFKLVTMQTAGNEIELENAADESKSEIDTLEMSSHDSGS 660
Qy 661 SLIRKSTRSVRSGSQDRKLSKEALDESIPVSVFWRIMKLNLTWPYVGVPCAIL 720
Db 661 SLIRKSTRSVRSGSQDRKLSKEALDESIPVSVFWRIMKLNLTWPYVGVPCAIL 720
Qy 721 NGGLQPAFVIFSKIIGIIFTRNDDEAKTRQNSNLSLLFLVLGIVSVITFPQFTFGKA 780
Db 721 NGGLQPAFVIFSKIIGIIFTRNDDEAKTRQNSNLSLLFLVLGIVSVITFPQFTFGKA 780
Qy 781 GEILTKELRYMFRSMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSRLLAITONI 840
Db 781 GEILTKELRYMFRSMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSRLLAITONI 840
Qy 841 ANLGTGIIISPIYCHQTLTLLLAIVPIIATAGVVMKLSQALXDKKELEGAGKIATEA 900
Db 841 ANLGTGIIISPIYCHQTLTLLLAIVPIIATAGVVMKLSQALXDKKELEGAGKIATEA 900
Qy 901 IENFRTVSVLTQEQKFEHMYDOSLOVPYRNSLRKAHIFGIIIFTSFTQAMMYSYAGCPRFG 960
Db 901 IENFRTVSVLTQEQKFEHMYAQSLOVPYRNSLRKAHIFGIIIFTSFTQAMMYSYAGCPRFG 960
Qy 961 AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIIEKTPILDS 1020
Db 961 AYLVAHKLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAAHIMIIIEKTPILDS 1020
Qy 1021 YSTGLKPNLTLEGNTVFNVEVFNYPTRDIPVLQGLSLFVKGGQTALVGSOGCKSTV 1080
Db 1021 YSTGLKPNLTLEGNTVFNVEVFNYPTRDIPVLQGLSLFVKGGQTALVGSOGCKSTV 1080
Qy 1081 QLLERFYDPLAGVLLDQKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENTAYGDSNRV 1140
Db 1081 QLLERFYDPLAGVLLDQKEIKRLNVQWMLRAHLGIVSQEPILFDCSIAENTAYGDSNRV 1140
Qy 1141 SOEETVRAAKEANIHAFTESLPNKYSTRVGDKGTQSGQKQRIARALVRQPHILLD 1200
Db 1141 SOEETVRAAKEANIHAFTESLPNKYSTRVGDKGTQSGQKQRIARALVRQPHILLD 1200
Qy 1201 EATSALDTESEKVVQEQALDKAREGTCIVIAHRLSTIQNADLIVVFQNGRVEKHTHOOL 1260
Db 1201 EATSALDTESEKVVQEQALDKAREGTCIVIAHRLSTIQNADLIVVFQNGRVEKHTHOOL 1260
Qy 1261 LAQKGIYFSMVSQAGAKRQ 1280
Db 1261 LAQKGIYFSMVSQAGTKRQ 1280

QY 1 MDLEGRNGAEKKNFKLANKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEKKNFKLANKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALL---TNSNITDTPVPMNLEEDMTRVAY 117
DB 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLFNNTNSNITDTPVPMNLEEDMTRVAY 120
QY 118 YSGIGAGVLAAYIOWSFVCLAAAGROTHKIRKQFPHAIMRQEIOWFVHDVDELNTRLT 177
DB 121 YSGIGAGVLAAYIOWSFVCLAAAGROTHKIRKQFPHAIMRQEIOWFVHDVDELNTRLT 180
QY 178 DVSKINEGIDGKIMGFQSMATFTFTGIVGTRGWLTLVLAIISPVLGLSAAVWAKILS 237
DB 181 DVSKINEGIDGKIMGFQSMATFTFTGIVGTRGWLTLVLAIISPVLGLSAAVWAKILS 240
QY 238 SPTDKELLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNKNLEAKRIGIKAITANI 297
DB 241 SPTDKELLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNKNLEAKRIGIKAITANI 300
QY 298 SIGAFLIYASALAFWYGTTLVLSEYSGOVLTVFFSVLIGAFSVGOASPSIEAPAN 357
DB 301 SIGAFLIYASALAFWYGTTLVLSEYSGOVLTVFFSVLIGAFSVGOASPSIEAPAN 360
QY 358 ARGAAFIKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHPSYPSRKEVKILKGLMLKV 417
DB 361 ARGAAFIKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHPSYPSRKEVKILKGLMLKV 420
QY 418 QSGQTVLVGNSGCKSTTVLMORLVDPTGMSVVDGODTIRTNVFLREIIGVSOEP 477
DB 421 QSGQTVLVGNSGCKSTTVLMORLVDPTGMSVVDGODTIRTNVFLREIIGVSOEP 480
QY 478 VLFATTAEIRYGRDVTMDIEIKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQK 537
DB 481 VLFATTAEIRYGRDVTMDIEIKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQK 540
QY 538 RIATARALVRNPKILLDEATSEALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
DB 541 RIATARALVRNPKILLDEATSEALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
QY 598 IAGFDGVIYKGNHDELMKGIYFKLVMTQAGNEIELENADESKSEIDTLEMSSH 657
DB 601 IAGFDGVIYKGNHDELMKGIYFKLVMTQAGNEIELENADESKSEIDTLEMSSH 660
QY 658 SGSSILRKSTRSRVSGQGDRLKSTKEALDESIPVPSFWIRIMKLNLTENPFYVGVFC 717
DB 661 SGSSILRKSTRSRVSGQGDRLKSTKEALDESIPVPSFWIRIMKLNLTENPFYVGVFC 720
QY 718 AINGGLQPAFAVIFSKIIGIFTRNDDAETKQNSNLSLLFLVLGIVSPTFFLQGTFF 777
DB 721 AINGGLQPAFAVIFSKIIGIFTRNDDAETKQNSNLSLLFLVLGIVSPTFFLQGTFF 780
QY 778 GKAGEILTKRLRYVFRSMLQDVSFDDPKNTTGALTTRLANDAAVKGAGSLAII 837
DB 781 GKAGEILTKRLRYVFRSMLQDVSFDDPKNTTGALTTRLANDAAVKGAGSLAII 840
QY 838 QNIANLGTGIIISLYGHQTLTLLAIPIAIAGVEMKMLSGQALKDKELEGAGKIA 897
DB 841 QNIANLGTGIIISLYGHQTLTLLAIPIAIAGVEMKMLSGQALKDKELEGAGKIA 900
QY 898 TEAIENFRVSLTQEQFEMHYDQSLQVPRNSLRKAIHIFGITSFTQAMMYFYAGCF 957
DB 901 TEAIENFRVSLTQEQFEMHYDQSLQVPRNSLRKAIHIFGITSFTQAMMYFYAGCF 960
QY 958 RFGAYLVASHLSMEDVLLVSAVVGAWAVGVSSPADYAKAVSAHIIIMIEKTP 1017
DB 961 RFGAYLVASHLSMEDVLLVSAVVGAWAVGVSSPADYAKAVSAHIIIMIEKTP 1020
QY 1018 IDSISTEGLKPNLTGNTFNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSSGCGKS 1077
DB 1021 IDSISTEGLKPNLTGNTFNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSSGCGKS 1080
QY 1078 TVVQLLERYDPLAGKVLDDGKEIKQLNVQWRAHLGIVSQBPILFDCSISENIAIGDNS 1137

DB 1081 TVVQLLERYDPLAGKVLDDGKEIKQLNVQWRAHLGIVSQBPILFDCSISENIAIGDNS 1140
QY 1138 RVVSQBEIVRAAKEANIHFIESLPNKYSTRVGDGKTQLSGGQKQRIATARALVROPHIL 1197
DB 1141 RVVSQBEIVRAAKEANIHFIESLPNKYSTRVGDGKTQLSGGQKQRIATARALVROPHIL 1200
QY 1198 LIDEATSAIDTSEKVVQVQALDKARGRCTIVIAHRLSTIONADLIVFQNGRVKEHGT 1257
DB 1201 LIDEATSAIDTSEKVVQVQALDKARGRCTIVIAHRLSTIONADLIVFQNGRVKEHGT 1260
QY 1258 QQLLAOKGIYFMSVSVQAGAKRQ 1280
DB 1261 QQLLAOKGIYFMSVSVQAGAKRQ 1283

RESULT 6

US-09-584-586-2

; Sequence 2, Application US/09584586

; Patent No. 633-3150

; GENERAL INFORMATION:

; APPLICANT: Sorrentino, Brian

; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH

; FILE REFERENCES: 1340-1-021CIP

; CURRENT APPLICATION NUMBER: US/09/584,586

; CURRENT FILING DATE: 2000-05-31

; EARLIER FILING DATE: 1998-05-28

; EARLIER FILING DATE: 1999-05-27

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 2

; LENGTH: 1280

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Human MDR 185-G

; US-09-584-586-2

Query Match 96.8%; Score 6218; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 123; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEKKNFKLANKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEKKNFKLANKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLTNSNITDTPVPMNLEEDMTRVAYYSG 120
DB 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLTNSNITDTPVPMNLEEDMTRVAYYSG 120
QY 121 IGAGLVAAIYQVSWFVCLAAAGROTHKIRKQFPHAIMRQEIOWFVHDVDELNTRLTDDVS 180
DB 121 IGAGLVAAIYQVSWFVCLAAAGROTHKIRKQFPHAIMRQEIOWFVHDVDELNTRLTDDVS 180
QY 181 KINEGIDGKIMGFQSMATFTFTGIVGTRGWLTLVLAIISPVLGLSAAVWAKILSFT 240
DB 181 KINEGIDGKIMGFQSMATFTFTGIVGTRGWLTLVLAIISPVLGLSAAVWAKILSFT 240
QY 241 DKEILLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNKNLEAKRIGIKAITANISIG 300
DB 241 DKEILLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNKNLEAKRIGIKAITANISIG 300
QY 301 AAFLLIYASALAFWYGTTLVLSEYSGOVLTVFFSVLIGAFSVGOASPSIEAFANAR 360
DB 301 AAFLLIYASALAFWYGTTLVLSEYSGOVLTVFFSVLIGAFSVGOASPSIEAFANAR 360
QY 361 AAFIFPKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKLKQSG 420
DB 361 AAFIFPKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKLKQSG 420

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; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2

Query Match      96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 1 MLEGGDRNGCAKKNFFKLNKSKKKKKKFTVSFVSFMSYNNWLDKLYMVVGTAAII 60
DB 1 1 MLEGGDRNGCAKKNFFKLNKSKKKKKKFTVSFVSFMSYNNWLDKLYMVVGTAAII 60
QY 61 HGAAGPLMLVFGDMTDFPANAGNIGDGLALLTNSNITDTVPVNNLEBDMTRYAYISG 120
DB 61 HGAAGPLMLVFGDMTDFPANAGNIGDGLALLTNSNITDTVPVNNLEBDMTRYAYISG 120
QY 121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKQFFHAIHQIHWDFVHDVDELNTRLTDDVS 180
DB 121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKQFFHAIHQIHWDFVHDVDELNTRLTDDVS 180
QY 181 KINEGIGDKIGMFFGOSMATFFTFGTFVGTGKWLTLVLAISPVLGLSAAVWAKILSSPT 240
DB 181 KINEVIGDKIGMFFGOSMATFFTFGTFVGTGKWLTLVLAISPVLGLSAAVWAKILSSPT 240
QY 241 DIELLAYAKAGAAVEEVLAAITVIAFGGKKELEKRYNNKLEAKRIGIKKAITANISIG 300
DB 241 DIELLAYAKAGAAVEEVLAAITVIAFGGKKELEKRYNNKLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASALAFYVGTTLVLKSEYSGOVLTVFVSFVLGAFSGQASPSIEAFANARG 360
DB 301 AAFLLIYASALAFYVGTTLVLKSEYSGOVLTVFVSFVLGAFSGQASPSIEAFANARG 360
QY 361 AAFEIFKIIDNKPSIDSYSGKHGKPDNIGKNEFRNVHPSYPSRKEVKILKGLNLKVQSG 420
DB 361 AAFEIFKIIDNKPSIDSYSGKHGKPDNIGKNEFRNVHPSYPSRKEVKILKGLNLKVQSG 420
QY 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGODITINVRFLREIIGVVSQEPVLV 480
DB 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGODITINVRFLREIIGVVSQEPVLV 480
QY 481 ATTIAENIRYGRNVTMDIEIKAVKEANAYDFIMKLPKFDTLVGERGAQLSGGQKORIA 540
DB 481 ATTIAENIRYGRNVTMDIEIKAVKEANAYDFIMKLPKFDTLVGERGAQLSGGQKORIA 540
QY 541 IARALVRNPKILLDEATSAIDTESAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSAIDTESAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVKGNHDELMEKEGIYFKLVMTQAGNEIENNADESKSEIDTLEMSHDSGS 660
DB 601 FDDGVIVKGNHDELMEKEGIYFKLVMTQAGNEIENNADESKSEIDTLEMSHDSGS 660
QY 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVVSFWRIMKLNLTWPYFVGVFCAII 720
DB 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVVSFWRIMKLNLTWPYFVGVFCAII 720
QY 721 NGGLQAPAFVIFSKIIGVTRIDDPETKQNSNLSLFLALGIIISFITFFLQGFPGA 780
DB 721 NGGLQAPAFVIFSKIIGVTRIDDPETKQNSNLSLFLALGIIISFITFFLQGFPGA 780
QY 781 GEILTRELRYVFRSMLRQDVSWDFDPKNTTGALTTRLANDAAQVKAIGSRILAITONI 840
DB 781 GEILTRELRYVFRSMLRQDVSWDFDPKNTTGALTTRLANDAAQVKAIGSRILAITONI 840
QY 841 ANLGTGIIISLIVGQWLTLLLAIVPIIAIAGVVMKQLSGOALDKKKELEGAGKATEA 900
DB 841 ANLGTGIIISLIVGQWLTLLLAIVPIIAIAGVVMKQLSGOALDKKKELEGAGKATEA 900
QY 901 IENFRVTLSQEQKPEHMYDQSLQVPRNSLRKAHIFGTFSTQAMTFFSVAGCPRFG 960
DB 901 IENFRVTLSQEQKPEHMYDQSLQVPRNSLRKAHIFGTFSTQAMTFFSVAGCPRFG 960
QY 961 AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIEKTPILDS 1020
DB 961 AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIEKTPILDS 1020
QY 1021 YSTEGLKPNLEGNVTNEVFNYPTRLDIPVLOGLSLEKKGQTLALVSSGCGKSTTV 1080
DB 1021 YSTEGLKPNLEGNVTNEVFNYPTRLDIPVLOGLSLEKKGQTLALVSSGCGKSTTV 1080
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DB 1081 QLLERFYDPLAGKVLDDKKEIKOLNVOLRAHLGIVSQEPIFPCSIENIAYGDSRVV 1140
QY 1141 SQEIVRAAKEANITHAFIESLPNKYSTRVGDKGTQLSGGQKORIAIARALVRPHILLD 1200
DB 1141 SQEIVRAAKEANITHAFIESLPNKYSTRVGDKGTQLSGGQKORIAIARALVRPHILLD 1200
QY 1201 EATSALDESKEVVOEALDKAREGTCIVIAHRLSTTONADLIVVFONGVKEHGTQOOL 1260
DB 1201 EATSALDESKEVVOEALDKAREGTCIVIAHRLSTTONADLIVVFONGVKEHGTQOOL 1260
QY 1261 LAQKGIYFSMVSVQAGAKRQ 1280
DB 1261 LAQKGIYFSMVSVQAGAKRQ 1280

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RESULT 7
US-09-767-594-2
; Sequence 2, Application US/09767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Bates, Susan
; APPLICANT: Robey, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Inhibition of MDR Transport by Acridine Derivatives

```

QY 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRQPHILLD 1200
 DB 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRQPHILLD 1200
 QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVRKEHGTQOL 1260
 DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVRKEHGTQOL 1260
 QY 1261 LAQKGIYFMSVMSVQAGTKRQ 1280
 DB 1261 LAQKGIYFMSVMSVQAGTKRQ 1280

RESULT 4

US-10-101-433A-5

; Sequence 5, Application US/10101433A

; Patent No. 6855812

; GENERAL INFORMATION:

; APPLICANT: Hanscom, Sara

; APPLICANT: Crespi, Charles

; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF

; FILE REFERENCE: G00307/70019

; CURRENT APPLICATION NUMBER: US/10/101,433A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: US 60/277,095

; PRIOR FILING DATE: 2001-03-19

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 1280

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-101-433A-5

Query Match 100.0%; Score 6431; DB 2; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGCAKKNFFKLNKSKKCKKPTVSFSPRYSNWLDKLYMVGTTAAII 60
 DB 1 MDLEGRNGCAKKNFFKLNKSKKCKKPTVSFSPRYSNWLDKLYMVGTTAAII 60

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 DB 61 HGAGLPLMLVFGEMTDIPANAGNLEDLMSNITNRSNDINTGPFMNLDEDMTRYAYYS 120

QY 121 IGAGVLVAAYIOVSFWCLAGROIHKIRKOPFHAIINROEIGWPDVHDVGEINRLTDDVS 180
 DB 121 IGAGVLVAAYIOVSFWCLAGROIHKIRKOPFHAIINROEIGWPDVHDVGEINRLTDDVS 180

QY 181 KINEVIGDKIGMFFQSMATFFTGFIIVGTRGKLTVLILAIISPLVGLSAVWAKILSSFT 240
 DB 181 KINEVIGDKIGMFFQSMATFFTGFIIVGTRGKLTVLILAIISPLVGLSAVWAKILSSFT 240

QY 241 DKELLAYAKAGAAVEVLAAITVTIAPGCKKELERYNNKLEAKRIGIKKAITANISIG 300
 DB 241 DKELLAYAKAGAAVEVLAAITVTIAPGCKKELERYNNKLEAKRIGIKKAITANISIG 300

QY 301 AAFLLIYASALAFWYGTTLVLSGYSIGOVLTVPFSLVIGAFSGVQASPSIEAFANARG 360
 DB 301 AAFLLIYASALAFWYGTTLVLSGYSIGOVLTVPFSLVIGAFSGVQASPSIEAFANARG 360

QY 361 AAYEIFIKIDNPKSIDYSKSGHPDNKGNLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
 DB 361 AAYEIFIKIDNPKSIDYSKSGHPDNKGNLEFRNVHFSYPSRKEVKILKGLNKVQSG 420

QY 421 QTVALVNSGCGKSTTQVMORLVDPTGEMVSDQDITINVRFLREIIGVSOEVLV 480
 DB 421 QTVALVNSGCGKSTTQVMORLVDPTGEMVSDQDITINVRFLREIIGVSOEVLV 480

QY 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKPDITLVGERGAQLSGGQKORIA 540

DB 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKPDITLVGERGAQLSGGQKORIA 540
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 DB 541 IABALVRNPKIILLDDATSAALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVRKEHGTQOL 600
 QY 601 FDDGVIVEKGNHDELMKEKGIYFKLVMTOTAGNEVELENADESKSEIDALEMSNDSRS 660
 DB 601 FDDGVIVEKGNHDELMKEKGIYFKLVMTOTAGNEVELENADESKSEIDALEMSNDSRS 660
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 DB 661 SLIRKSTRRSVRGSOAQRKSLSTKEALDESIPVSWRIMKLNLTENPFYVGVFCAL 720
 QY 721 NGGLQPAFALIFSKIIIGVFTTRIDDPETKRONSLFSLFLALGIIISFTTFPLOGTFFGKA 780
 DB 721 NGGLQPAFALIFSKIIIGVFTTRIDDPETKRONSLFSLFLALGIIISFTTFPLOGTFFGKA 780
 QY 781 GEILTKRLRYMVRSMRLRQDVSWFDDPKNTTGALTTRLANDAAOVKGAIGSLRAVITONI 840
 DB 781 GEILTKRLRYMVRSMRLRQDVSWFDDPKNTTGALTTRLANDAAOVKGAIGSLRAVITONI 840
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 DB 841 ANLCTGIIISFIYQWLTLLLAIVPIIAIAGVVEMLSGQALKKKELEGAGKIATEA 900
 QY 901 IENFRTVVSLTQEQPEHMAQSIQVFPYNSLRKAHIFGITFTFTQMMYFSYAGCFRFG 960
 DB 901 IENFRTVVSLTQEQPEHMAQSIQVFPYNSLRKAHIFGITFTFTQMMYFSYAGCFRFG 960
 QY 961 AYLVAHKLMSEFEDVLLVFSVAVFGMAVGVQVSPFADYAKAKISAAHIMIIEKTPILDS 1020
 DB 961 AYLVAHKLMSEFEDVLLVFSVAVFGMAVGVQVSPFADYAKAKISAAHIMIIEKTPILDS 1020

QY 1021 YSTEGMLPNTLEGNTVTFGEVWYPRDIPVQLGLEVKKGOTLALVSSGCGKSTV 1080
 DB 1021 YSTEGMLPNTLEGNTVTFGEVWYPRDIPVQLGLEVKKGOTLALVSSGCGKSTV 1080

QY 1081 QLLERFYDPLAGKVLIDGKEIKRLNVQMLRAHLGIVSOEPIFLDCSIAENIAYGNSRV 1140
 DB 1081 QLLERFYDPLAGKVLIDGKEIKRLNVQMLRAHLGIVSOEPIFLDCSIAENIAYGNSRV 1140

QY 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRQPHILLD 1200
 DB 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRQPHILLD 1200

QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVRKEHGTQOL 1260
 DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVRKEHGTQOL 1260

QY 1261 LAQKGIYFMSVMSVQAGTKRQ 1280
 DB 1261 LAQKGIYFMSVMSVQAGTKRQ 1280

RESULT 5

US-09-817-762-3

; Sequence 3, Application US/09817762

; Patent No. 6858724

; GENERAL INFORMATION:

; APPLICANT: Spalding, Edgar P.

; APPLICANT: No. 6858774, Bost.

; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 13238-00061

; CURRENT APPLICATION NUMBER: US/09/817,762

; CURRENT FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: PCT/US99/22363

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: US 60/101,814

; PRIOR FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0


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; SEQ ID NO 3
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION.
; DATABASE ACCESSION NUMBER: Genbank P08183
; DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match      100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGGAKKQNFKKLNKSEKDKKPKTTSVFSMFRYSNMLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAKKQNFKKLNKSEKDKKPKTTSVFSMFRYSNMLDKLYMVVGTAAII 60
QY 61 HGAGLPLMWLVFGEMTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
DB 61 HGAGLPLMWLVFGEMTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
QY 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIIGWDFVDHVGELNTRLTDDVS 180
DB 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIIGWDFVDHVGELNTRLTDDVS 180
QY 181 KINEVIGDKIGMFFQSMATFTTGFIVGTRGWKLTIVILAIISPVLGLSAAVWAKILSPT 240
DB 181 KINEVIGDKIGMFFQSMATFTTGFIVGTRGWKLTIVILAIISPVLGLSAAVWAKILSPT 240
QY 241 KELLAYAKAGAVAEVLAAITVTAFGGKKELERYNKNLEAKRIGIKKAITANISIG 300
DB 241 KELLAYAKAGAVAEVLAAITVTAFGGKKELERYNKNLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASYALAFYGTTLVLSGEYSIGQVLTVPFSLVIGAFSGVQASPSIEAFANARG 360
DB 301 AAFLLIYASYALAFYGTTLVLSGEYSIGQVLTVPFSLVIGAFSGVQASPSIEAFANARG 360
QY 361 AAYEIFKIIDNPKSIDSYSGSKGHPDNINKNLEFRNVHPSYPSRKEVKILGKLNKVQSG 420
DB 361 AAYEIFKIIDNPKSIDSYSGSKGHPDNINKNLEFRNVHPSYPSRKEVKILGKLNKVQSG 420
QY 421 QTVALVGNSSGCKSTTVQMLQRLYDPTGEMVSDGQDITINVRFLREIIGVVSQEPVLV 480
DB 421 QTVALVGNSSGCKSTTVQMLQRLYDPTGEMVSDGQDITINVRFLREIIGVVSQEPVLV 480
QY 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIA 540
DB 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 PDGIVIVKGNHDELMKEGIFVKLTVMQTAGNEVELENADESKEIDALESSNDSRS 660
DB 601 PDGIVIVKGNHDELMKEGIFVKLTVMQTAGNEVELENADESKEIDALESSNDSRS 660
QY 661 SLIRKSTRSRVSGQAQDRKLTKEALDESIPVSWFRIMKLNLTWEPYFVGVVPCAI 720
DB 661 SLIRKSTRSRVSGQAQDRKLTKEALDESIPVSWFRIMKLNLTWEPYFVGVVPCAI 720
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DB 721 NGGLOPAPAFIIFSKLIGVTRIDDDPETKQNSNLSLLFLAIGIISFITFLOGTFGKA 780
QY 781 GBILTKRLRYMYFRSMLRQDWSWFDPKNTTGALTTRLANDAAQVKAIGSLAVITQNI 840
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DB 841 ANLGTGIIISFYGWQLTLLLAIVPIIAIAGVVENKMLSGQALKDQKLEGGAGKIATEA 900

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QY 961 AYLVAHKLMSPEDVLLVFSVVFQAMAVGVSSPAPYAKAKISAAHIIMIIEKTPILDS 1020
DB 961 AYLVAHKLMSPEDVLLVFSVVFQAMAVGVSSPAPYAKAKISAAHIIMIIEKTPILDS 1020
QY 1021 YSTGLMPTNLTGNTVTFGEVVFNPTPRDIPVLOGLSLEVKKGOTLALVSSGCGKSTVV 1080
DB 1021 YSTGLMPTNLTGNTVTFGEVVFNPTPRDIPVLOGLSLEVKKGOTLALVSSGCGKSTVV 1080
QY 1081 QLLERFYDPLAGKVLDDGKEIKRLNVQWLAHLGIVSOEPIFLDCSIAENIAYGDSRVV 1140
DB 1081 QLLERFYDPLAGKVLDDGKEIKRLNVQWLAHLGIVSOEPIFLDCSIAENIAYGDSRVV 1140
QY 1141 SOEIVRAAKEANTHAFIESLPNKYSTKVGDKGTQSGQKQRIARALVRQPHILLD 1200
DB 1141 SOEIVRAAKEANTHAFIESLPNKYSTKVGDKGTQSGQKQRIARALVRQPHILLD 1200
QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVFQNGRVKEHGTQOOL 1260
DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVFQNGRVKEHGTQOOL 1260
QY 1261 LAQKGIYFSMVSVQAGTKRQ 1280
DB 1261 LAQKGIYFSMVSVQAGTKRQ 1280

RESULT 6
US-09-584-586-4
; Sequence 4, Application US/09584586
; Patent No. 6533150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
US-09-584-586-4

Query Match      100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGGAKKQNFKKLNKSEKDKKPKTTSVFSMFRYSNMLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAKKQNFKKLNKSEKDKKPKTTSVFSMFRYSNMLDKLYMVVGTAAII 60
QY 61 HGAGLPLMWLVFGEMTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
DB 61 HGAGLPLMWLVFGEMTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
QY 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIIGWDFVDHVGELNTRLTDDVS 180
DB 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIIGWDFVDHVGELNTRLTDDVS 180
QY 181 KINEVIGDKIGMFFQSMATFTTGFIVGTRGWKLTIVILAIISPVLGLSAAVWAKILSPT 240
DB 181 KINEVIGDKIGMFFQSMATFTTGFIVGTRGWKLTIVILAIISPVLGLSAAVWAKILSPT 240
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Db 181 KINEVIGDKIGMFQSQMATFTGTFVGTGKWKUTLVILAIKSPVLGSAVWAKILSSFT 240
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Db 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIIVASALAFWYGTTLVLSEYSGVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Db 301 AAFLLIIVASALAFWYGTTLVLSEYSGVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
QY 361 AAYEIFIKIDNKPISIDSKSGHKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKLKQSG 420
Db 361 AAYEIFIKIDNKPISIDSKSGHKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKLKQSG 420
QY 421 QTVALVNSGCGKSTTVOLMORLYDPTGEMVSDQDINTINNVRLREIIGVVSQBPVLF 480
Db 421 QTVALVNSGCGKSTTVOLMORLYDPTGEMVSDQDINTINNVRLREIIGVVSQBPVLF 480
QY 481 ATTIAENIRYGRNVWDEIEKAVEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
Db 481 ATTIAENIRYGRNVWDEIEKAVEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
QY 541 IARALVENPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVENPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIIVEKGNHDELMKEGKIYFKLVMTQTAGNEVELENAADESKSIDALENSNDNRS 660
Db 601 FDDGVIIVEKGNHDELMKEGKIYFKLVMTQTAGNEVELENAADESKSIDALENSNDNRS 660
QY 661 SLIKRSTRSVRSGOQDRKLSKEALDSEIPVPSFWRIMKMLNLTWPVYVGVFCAIL 720
Db 661 SLIKRSTRSVRSGOQDRKLSKEALDSEIPVPSFWRIMKMLNLTWPVYVGVFCAIL 720
QY 721 NGGLQPAFAIIFSKIIIGVFRIDDPETKRONSNLFSLLFLALGIISITFFLQGFTEGKA 780
Db 721 NGGLQPAFAIIFSKIIIGVFRIDDPETKRONSNLFSLLFLALGIISITFFLQGFTEGKA 780
QY 781 GEILTUKRLRYVFRSMRLQDVSWPDDPNTTGTALTTRLANDAQAQVGAIGSRSLAVITQNI 840
Db 781 GEILTUKRLRYVFRSMRLQDVSWPDDPNTTGTALTTRLANDAQAQVGAIGSRSLAVITQNI 840
QY 841 ANLGTGIIISFIYGMQTLTLLALVPIIAIAGVVMKMLSGOALKDKKELEGAGKATEA 900
Db 841 ANLGTGIIISFIYGMQTLTLLALVPIIAIAGVVMKMLSGOALKDKKELEGAGKATEA 900
QY 901 IENFRVTVSLTQEQKFEMHYAQSLQVPRNSLRKAHIFGITFSTQAMMYFSYAGCFRFG 960
Db 901 IENFRVTVSLTQEQKFEMHYAQSLQVPRNSLRKAHIFGITFSTQAMMYFSYAGCFRFG 960
QY 961 AYLVAKHKLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAHHIMIEKTPILDS 1020
Db 961 AYLVAKHKLMSFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAHHIMIEKTPILDS 1020
QY 1021 YSTEGMLPNTLEGNTVFEVVFNTPRDPDIPVQLGSLVKKGOTLALVSGSGCGKSTVV 1080
Db 1021 YSTEGMLPNTLEGNTVFEVVFNTPRDPDIPVQLGSLVKKGOTLALVSGSGCGKSTVV 1080
QY 1081 QLLERFYDPLAGKYLLDGKEIKRLNVQWLAHGLIGVSOEPILPDCSIAENIAYGDNRRV 1140
Db 1081 QLLERFYDPLAGKYLLDGKEIKRLNVQWLAHGLIGVSOEPILPDCSIAENIAYGDNRRV 1140
QY 1141 SOBEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGOKORTIARALVRPHILLD 1200
Db 1141 SOBEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGOKORTIARALVRPHILLD 1200
QY 1201 EATSALDTESEKVVQEAALDKAREGRTCTIVIAHRLSTIQNADLIWVFONGRVKRGHTHOQL 1260
Db 1201 EATSALDTESEKVVQEAALDKAREGRTCTIVIAHRLSTIQNADLIWVFONGRVKRGHTHOQL 1260
QY 1261 LAQKGIYFMSVSVQAGTKRQ 1280
Db 1261 LAQKGIYFMSVSVQAGTKRQ 1280

RESULT 7

US-08-583-276-19

; Sequence 19, Application US/08583276

; Patent No. 5837536

; GENERAL INFORMATION:

; APPLICANT: McDonagh, Kevin T.

; APPLICANT: Nienhuis, Arthur

; APPLICANT: Tolstoshev, Paul

; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN

; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED

; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi & Stewart

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: DW4.V2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,276

; FILING DATE: 05-JAN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/332,444

; FILING DATE: 31-OCT-1994

; APPLICATION NUMBER: 07/897,712

; FILING DATE: 22-MAY-1992

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1280 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: protein

; US-08-583-276-19

Query Match 99.9%; Score 6428; DB 1; Length 1280;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEGDRNGGAKKQKFFKLNKSEKDKKPKTVSVFMSFRYSNNWLDKLYMVVGTAAII 60

Db 1 MDEGDRNGGAKKQKFFKLNKSEKDKKPKTVSVFMSFRYSNNWLDKLYMVVGTAAII 60

QY 61 HGAGLPLMLVFGEMTDIFANAGNLEDLSNITNRSINDTGFNNLBEDMTRYAYISG 120

Db 61 HGAGLPLMLVFGEMTDIFANAGNLEDLSNITNRSINDTGFNNLBEDMTRYAYISG 120

QY 121 IGAGLVAAIYQVSWFCLAAAGROIHKIRKQFFHAIHQEIGWDFVDVHDLNTRLTDDVS 180

Db 121 IGAGLVAAIYQVSWFCLAAAGROIHKIRKQFFHAIHQEIGWDFVDVHDLNTRLTDDVS 180

QY 181 KINEVIGDKIGMFFQSQMATFTGTFVGTGKWKUTLVILAIKSPVLGSAVWAKILSSFT 240

Db 181 KINEVIGDKIGMFFQSQMATFTGTFVGTGKWKUTLVILAIKSPVLGSAVWAKILSSFT 240

QY 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANISIG 300

Db 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANISIG 300

QY 301 AAFLLIIVASALAFWYGTTLVLSEYSGVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360

Db 301 AAFLLIIVASALAFWYGTTLVLSEYSGVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360

1 MDLEGRNGGAEKKNFFKLNKSKODKCKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
1 MDLEGRNGGAEKKNFFKLNKSKODKCKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
61 HGAGLPLMLVFGDMTDTFANAGNLDGALLFNNTSSNITDTVPVNNLEEDMTRYAY 120
61 HGAGLPLMLVFGDMTDTFANAGNLDGALLFNNTSSNITDTVPVNNLEEDMTRYAY 117
121 YSGIGAGVLAAYTQVSWFCLAAAGQIHKIRKOPFHAIHQEIGFDFVHDVDELNTRLD 180
118 YSGIGAGVLAAYTQVSWFCLAAAGQIHKIRKOPFHAIHQEIGFDFVHDVDELNTRLD 177
181 DVSKINEGIDGKIMGFFOSMATFTFTGFTVTRGWKLTVLILAIISPVLSAAVWAKILS 240
178 DVSKINEGIDGKIMGFFOSMATFTFTGFTVTRGWKLTVLILAIISPVLSAAVWAKILS 237
241 SFTDKELLAYAKAGAAVEVLAAIRTVIAPGGOKKELRYNNKLEAKRIGIKKAITANI 300
238 SFTDKELLAYAKAGAAVEVLAAIRTVIAPGGOKKELRYNNKLEAKRIGIKKAITANI 297
301 SIGAAFLIIYASALAFWYGTTLVLSKEYSIGQVLTVPFSSVLIGAFSGVGOASPIEAFAN 360
298 SIGAAFLIIYASALAFWYGTTLVLSKEYSIGQVLTVPFSSVLIGAFSGVGOASPIEAFAN 357
361 ARGAAAFIFKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
358 ARGAAAFIFKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
421 QSGQTVALVGNSSGCKSTTVOLMRLYDPTGEGVSDGQDINTINVRFLRIIIGVVSQEP 480
418 QSGQTVALVGNSSGCKSTTVOLMRLYDPTGEGVSDGQDINTINVRFLRIIIGVVSQEP 477
481 VLFATTAEINRYGREDVTWDEIEKAVKEANAYDFIMKLPQKFDTLVGERGAOLSGGQK 540
478 VLFATTAEINRYGREDVTWDEIEKAVKEANAYDFIMKLPQKFDTLVGERGAOLSGGQK 537
541 RIATARALVRNPKILLDEATSAIDTSEAVVQVADKARKGRITIVIAHRLSTVRNADV 600
538 RIATARALVRNPKILLDEATSAIDTSEAVVQVADKARKGRITIVIAHRLSTVRNADV 597
601 IAGDDGIVIVKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHD 660
598 IAGDDGIVIVKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHD 657
661 SGSLIRKSTRSRVSGQDRKLSKEALDESIPVPSFRIMKLNLTENPYPFVGVFC 720
658 SGSLIRKSTRSRVSGQDRKLSKEALDESIPVPSFRIMKLNLTENPYPFVGVFC 717
721 AIINGGLQPAFAVIFSKIIIGITRNDDAETKRONSLFSLFLVIGIVSFITFLQGF 780
718 AIINGGLQPAFAVIFSKIIIGITRNDDAETKRONSLFSLFLVIGIVSFITFLQGF 777
781 KGAGEILTTLRYVMVFRSMLRQDSWFDPPKNTTGALTTRLANDAAQVKGAGISRLAIT 840
778 KGAGEILTTLRYVMVFRSMLRQDSWFDPPKNTTGALTTRLANDAAQVKGAGISRLAIT 837
841 QNIANLGTGIIISLYGHQTLILLAIIVPIIAGVEMKMLSGQALDKKKELEGAGKIA 900
838 QNIANLGTGIIISLYGHQTLILLAIIVPIIAGVEMKMLSGQALDKKKELEGAGKIA 897
901 TEATENRTVSLTQEQFHEMYDOSLOVPYRNSLRKAHIFGITFSTQAMMYFSYACGF 960
898 TEATENRTVSLTQEQFHEMYDOSLOVPYRNSLRKAHIFGITFSTQAMMYFSYACGF 957
961 RFGAYLVAHLSMEDVLLVFSVAVFGAMAVGQVSSPAPDYAKAKVSAHIIIMIEKTPL 1020
958 RFGAYLVAHLSMEDVLLVFSVAVFGAMAVGQVSSPAPDYAKAKVSAHIIIMIEKTPL 1017
1021 IDSYSTGLKNTLEGNTVNEVFNPTRLDIPVLQGLSLEVKKGOTLALVSGSGCKS 1080
1018 IDSYSTGLKNTLEGNTVNEVFNPTRLDIPVLQGLSLEVKKGOTLALVSGSGCKS 1077
1081 TVVQLLRFYDPLAGKVLDDKEIKQLNVQWRAHLGIVSQEPILFDCSISENTAYGNS 1140

1078 TVVQLLRFYDPLAGKVLDDKEIKQLNVQWRAHLGIVSQEPILFDCSISENTAYGNS 1137
1141 RVWSQEBIVRAAKKANTHAFIESLPNKYSTRVGDKGTQSGQKORIAIARALVROPHIL 1200
1138 RVWSQEBIVRAAKKANTHAFIESLPNKYSTRVGDKGTQSGQKORIAIARALVROPHIL 1197
1201 LLDDEATSAIDTSEKVVQVEALDKAREGRTCTIVIAHRLSTQIADLIIVFQNGRVKEHGH 1260
1198 LLDDEATSAIDTSEKVVQVEALDKAREGRTCTIVIAHRLSTQIADLIIVFQNGRVKEHGH 1257
1261 QQLLAQKGIYFSMVSVQAGAKRQ 1283
1258 QQLLAQKGIYFSMVSVQAGAKRQ 1280
RESULT 6
US-09-584-586-2
; Sequence 2, Application US/09584586
; Patent No. 6933150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-G
US-09-584-586-2
Query Match 96.4%; Score 6212.5; DB 2; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1238; Conservative 18; Mismatches 24; Indels 3; Gaps 1;
QY 1 MDLEGRNGGAEKKNFFKLNKSKODKCKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGGAEKKNFFKLNKSKODKCKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLDGALLFNNTSSNITDTVPVNNLEEDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLDGALLFNNTSSNITDTVPVNNLEEDMTRYAY 117
QY 121 YSGIGAGVLAAYTQVSWFCLAAAGQIHKIRKOPFHAIHQEIGFDFVHDVDELNTRLD 180
DB 118 YSGIGAGVLAAYTQVSWFCLAAAGQIHKIRKOPFHAIHQEIGFDFVHDVDELNTRLD 177
QY 181 DVSKINEGIDGKIMGFFOSMATFTFTGFTVTRGWKLTVLILAIISPVLSAAVWAKILS 240
DB 178 DVSKINEGIDGKIMGFFOSMATFTFTGFTVTRGWKLTVLILAIISPVLSAAVWAKILS 237
QY 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAPGGOKKELRYNNKLEAKRIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAPGGOKKELRYNNKLEAKRIGIKKAITANI 297
QY 301 SIGAAFLIIYASALAFWYGTTLVLSKEYSIGQVLTVPFSSVLIGAFSGVGOASPIEAFAN 360
DB 298 SIGAAFLIIYASALAFWYGTTLVLSKEYSIGQVLTVPFSSVLIGAFSGVGOASPIEAFAN 357
QY 361 ARGAAAFIFKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
DB 358 ARGAAAFIFKIIDNKPSIDSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417

421 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDRTINVRFLREIIGVVSQBP 480
418 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDRTINVRFLREIIGVVSQBP 477
481 VLFATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPOKFDTLVGERGQALSGGQK 540
478 VLFATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPHKFDTLVGERGQALSGGQK 537
541 RTAIALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
538 RTAIALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
601 IAGFDGVTVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSND 660
598 IAGFDGVTVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSND 657
661 SSSLIIRKSTRSRVRSVRSQQRKLTKEALDESIPVPSFWIMKLNLTWFFVVGVC 720
658 SRSSLIIRKSTRSRVRSVRSQQRKLTKEALDESIPVPSFWIMKLNLTWFFVVGVC 717
721 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSLFLALGIIISFIIFLQGF 780
718 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSLFLALGIIISFIIFLQGF 777
781 GKAGELTKRLRYMFRSMRLRODVSMFDDPKNTTGALTTRLANDAAQVKAIGSLAIT 840
778 GKAGELTKRLRYMFRSMRLRODVSMFDDPKNTTGALTTRLANDAAQVKAIGSLAIT 837
841 QNIANLGTGIIISLIYWGQVTLTLLLAIVPIIAIAGVEMKMLSGQALKDKKELEGAK 900
838 QNIANLGTGIIISLIYWGQVTLTLLLAIVPIIAIAGVEMKMLSGQALKDKKELEGAK 897
901 TEAIENFRVTSLTQKQEHYVQSLQVLPYRNSLRKAHIFGTFSTQAMVFSYAGCF 960
898 TEAIENFRVTSLTQKQEHYVQSLQVLPYRNSLRKAHIFGTFSTQAMVFSYAGCF 957
961 RFGAYLVHSLMSFEDVLVFSVAVFGMAVGVSSFPADYAKAKVSAAHITMIIEKTP 1020
958 RFGAYLVHSLMSFEDVLVFSVAVFGMAVGVSSFPADYAKAKVSAAHITMIIEKTP 1017
1021 IDSYSTGLKPNTEGNTVFNEVFNPTRLDIPVLQGLSLEVKVQGTALVGSQCGKS 1080
1018 IDSYSTGLKPNTEGNTVFNEVFNPTRLDIPVLQGLSLEVKVQGTALVGSQCGKS 1077
1081 TVVQLLERYFDPLAGKVLDDGKEIKOLNVQWLBRAHIGIYVSOEPILPDCSTENIAGD 1140
1078 TVVQLLERYFDPLAGKVLDDGKEIKOLNVQWLBRAHIGIYVSOEPILPDCSTENIAGD 1137
1141 RVVSOEIVRAAKEANIHAFIESLPNKYSTRVGDKGTQLSGGQKRIATARALVRPHIL 1200
1138 RVVSOEIVRAAKEANIHAFIESLPNKYSTRVGDKGTQLSGGQKRIATARALVRPHIL 1197
1201 LLDDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 1260
1198 LLDDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 1257
1261 QQLLAQGIYFMSVQAGAKRQ 1283
1258 QQLLAQGIYFMSVQAGAKRQ 1280

RESULT 7
US-09-767-594-2
; Sequence 2, Application US/09767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Bates, Susan
; APPLICANT: Robey, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
QY 1 MDLEGRNGCAEKKNFFKLNKSKKDKKERKPTVSVFMSFRYSNWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGCAEKKNFFKLNKSKKDKKERKPTVSVFMSFRYSNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNIGDGLGALLFNNTSSNITDTPVNVNLEDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNIGDGLGALLFNNTSSNITDTPVNVNLEDMTRYAY 117
QY 121 YSGIGAGVVAAYIOVSFWCLAAAGROIHKIRKQPHFAMROEIGWDFVDHVGELNRLTD 180
DB 118 YSGIGAGVVAAYIOVSFWCLAAAGROIHKIRKQPHFAMROEIGWDFVDHVGELNRLTD 177
QY 181 DVSKINEGIDKIGNFFQSMATFFTGIVGTGKMLTLVILAIISPVLGSAAVWAKILS 240
DB 178 DVSKINEGIDKIGNFFQSMATFFTGIVGTGKMLTLVILAIISPVLGSAAVWAKILS 237
QY 241 SFTDKELLAYAKAGAVAEVLAARTVIAFGOKKELERYKNLEERKIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAVAEVLAARTVIAFGOKKELERYKNLEERKIGIKKAITANI 297
QY 301 SIGAFLIYASALAFWYGTTLVLSKEYSIOGVLTVPFVSVLIGAFSGQASPSIEAFAN 360
DB 298 SIGAFLIYASALAFWYGTTLVLSKEYSIOGVLTVPFVSVLIGAFSGQASPSIEAFAN 357
QY 361 ARGAAFEIKIIDNKPSIDSYSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLN 420
DB 358 ARGAAFEIKIIDNKPSIDSYSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLN 417
QY 421 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDRTINVRFLREIIGVVSQBP 480
DB 418 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDRTINVRFLREIIGVVSQBP 477
QY 481 VLFATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPOKFDTLVGERGQALSGGQK 540
DB 478 VLFATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPHKFDTLVGERGQALSGGQK 537
QY 541 RTAIALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RTAIALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGFDGVTVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSND 660
DB 598 IAGFDGVTVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSND 657
QY 661 SSSLIIRKSTRSRVRSVRSQQRKLTKEALDESIPVPSFWIMKLNLTWFFVVGVC 720
DB 658 SRSSLIIRKSTRSRVRSVRSQQRKLTKEALDESIPVPSFWIMKLNLTWFFVVGVC 717
QY 721 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSLFLALGIIISFIIFLQGF 780
DB 718 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSLFLALGIIISFIIFLQGF 777

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 MDLEGRNGGAKGNFFKLNKSKDKKPKPTVSFMSFRYSNMWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAKGNFFKLNKSKDKKPKPTVSFMSFRYSNMWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTPVPMNLEEDMTRYAY 120
DB 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTPVPMNLEEDMTRYAY 117
QY 121 YSGIGAGVLVAAYIQVSFWCLAGROHQHKKIRKQFPHAIMRQEIQWDFVHDVHVGELNTRLTD 180
DB 118 YSGIGAGVLVAAYIQVSFWCLAGROHQHKKIRKQFPHAIMRQEIQWDFVHDVHVGELNTRLTD 177
QY 181 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAAVWAKILS 240
DB 178 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAAVWAKILS 237
QY 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKGIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKGIGIKKAITANI 297
QY 301 SIGAELLIIYASALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 360
DB 298 SIGAELLIIYASALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 357
QY 361 ARGAAFEIKIINDKPSIDSYSGSHKPNKGNLEFRNVHFSYPSRKEVKILKGNLKV 420
DB 358 ARGAAFEIKIINDKPSIDSYSGSHKPNKGNLEFRNVHFSYPSRKEVKILKGNLKV 417
QY 421 QSGQTVALVGNSSCGSTTVQLMORLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 480
DB 418 QSGQTVALVGNSSCGSTTVQLMORLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 477
QY 481 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 540
DB 478 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 537
QY 541 RIAIARALVNPKILLDEATSDLTSEAVQVVALDKARKGRTTIVIAHRLSTVNRADV 600
DB 538 RIAIARALVNPKILLDEATSDLTSEAVQVVALDKARKGRTTIVIAHRLSTVNRADV 597
QY 601 IAGFDDGVIVKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSHD 660
DB 598 IAGFDDGVIVKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSHD 657
QY 661 SGSSLRKSTRSVRSGSQDRKLSLTKALDESIPPVSWFRIMKMLNLTWPYFVGVFC 720
DB 658 SRSLRKSTRSVRSGSQDRKLSLTKALDESIPPVSWFRIMKMLNLTWPYFVGVFC 717
QY 721 AIINGGLOPAVIFSKIIGIFTRNDADYTRQNSNLFSLFLVLGVISFITPFGQFTF 780
DB 718 AIINGGLOPAVIFSKIIGIFTRNDADYTRQNSNLFSLFLVLGVISFITPFGQFTF 777
QY 781 GKAGEILTCLRVMVPSMLRQDVSFDDPKNTTGALTTRLANDAAVKGAISRLAIIIT 840
DB 778 GKAGEILTCLRVMVPSMLRQDVSFDDPKNTTGALTTRLANDAAVKGAISRLAIIIT 837
QY 841 QNTANLGTGIIISLIYQWQLTLLALLAIVPIIATAGVVMKMLSGOALKDKKELEGAGKIA 900
DB 838 QNTANLGTGIIISLIYQWQLTLLALLAIVPIIATAGVVMKMLSGOALKDKKELEGAGKIA 897
QY 901 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITPFSFQAMMYSYAGCF 960
DB 898 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITPFSFQAMMYSYAGCF 957
QY 961 RFGAYLVAHLSMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVAAHIIIMIEKTP 1020
DB 958 RFGAYLVAHLSMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVAAHIIIMIEKTP 1017
QY 1021 IDSYSTEGLKNTLEGNVTFNEVFNPTRLDIPVLOGLSLEVKKGTALVGSSSGCGKS 1080

1018 IDSYSTEGLKNTLEGNVTFNEVFNPTRLDIPVLOGLSLEVKKGTALVGSSSGCGKS 1077
1081 TVVQLLEFYDPLAGKVLDDGKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENTIAYGNS 1140
1078 TVVQLLEFYDPLAGKVLDDGKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENTIAYGNS 1137
1141 RVVSOEEIVRAAKENIAHAFIESLPNKYSTRVGDKGTOLSGGOKORIAIARALVROPHIL 1200
1138 RVVSOEEIVRAAKENIAHAFIESLPNKYSTRVGDKGTOLSGGOKORIAIARALVROPHIL 1197
1201 LIDEATSDLTSEKVVQVQALDKAREGTCIVIAHRLSTIONADLIVVFQNGRVKHEGTH 1260
1198 LIDEATSDLTSEKVVQVQALDKAREGTCIVIAHRLSTIONADLIVVFQNGRVKHEGTH 1257
1261 QOLLAQKGIYFSWVSVOAGAKRQ 1283
1258 QOLLAQKGIYFSWVSVOAGAKRQ 1280

RESULT 11
US-09-817-762-3
Sequence 3, Application US/09817762
Patent No. 6958774
GENERAL INFORMATION
APPLICANT: Spalding, Edgar P.
APPLICANT: No. 6858774, Bostl
TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
TITLE OF INVENTION: Plants
FILE REFERENCE: 13238-00061
CURRENT APPLICATION NUMBER: US/09/817,762
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: PCT/US99/22363
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,814
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank P08183
DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 MDLEGRNGGAKGNFFKLNKSKDKKPKPTVSFMSFRYSNMWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAKGNFFKLNKSKDKKPKPTVSFMSFRYSNMWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTPVPMNLEEDMTRYAY 120
DB 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTPVPMNLEEDMTRYAY 117
QY 121 YSGIGAGVLVAAYIQVSFWCLAGROHQHKKIRKQFPHAIMRQEIQWDFVHDVHVGELNTRLTD 180
DB 118 YSGIGAGVLVAAYIQVSFWCLAGROHQHKKIRKQFPHAIMRQEIQWDFVHDVHVGELNTRLTD 177
QY 181 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAAVWAKILS 240
DB 178 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAAVWAKILS 237
QY 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKGIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKGIGIKKAITANI 297
QY 301 SIGAELLIIYASALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 360
DB 298 SIGAELLIIYASALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 357
QY 361 ARGAAFEIKIINDKPSIDSYSGSHKPNKGNLEFRNVHFSYPSRKEVKILKGNLKV 420
DB 358 ARGAAFEIKIINDKPSIDSYSGSHKPNKGNLEFRNVHFSYPSRKEVKILKGNLKV 417
QY 421 QSGQTVALVGNSSCGSTTVQLMORLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 480
DB 418 QSGQTVALVGNSSCGSTTVQLMORLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 477
QY 481 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 540
DB 478 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 537
QY 541 RIAIARALVNPKILLDEATSDLTSEAVQVVALDKARKGRTTIVIAHRLSTVNRADV 600
DB 538 RIAIARALVNPKILLDEATSDLTSEAVQVVALDKARKGRTTIVIAHRLSTVNRADV 597
QY 601 IAGFDDGVIVKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSHD 660
DB 598 IAGFDDGVIVKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSHD 657
QY 661 SGSSLRKSTRSVRSGSQDRKLSLTKALDESIPPVSWFRIMKMLNLTWPYFVGVFC 720
DB 658 SRSLRKSTRSVRSGSQDRKLSLTKALDESIPPVSWFRIMKMLNLTWPYFVGVFC 717
QY 721 AIINGGLOPAVIFSKIIGIFTRNDADYTRQNSNLFSLFLVLGVISFITPFGQFTF 780
DB 718 AIINGGLOPAVIFSKIIGIFTRNDADYTRQNSNLFSLFLVLGVISFITPFGQFTF 777
QY 781 GKAGEILTCLRVMVPSMLRQDVSFDDPKNTTGALTTRLANDAAVKGAISRLAIIIT 840
DB 778 GKAGEILTCLRVMVPSMLRQDVSFDDPKNTTGALTTRLANDAAVKGAISRLAIIIT 837
QY 841 QNTANLGTGIIISLIYQWQLTLLALLAIVPIIATAGVVMKMLSGOALKDKKELEGAGKIA 900
DB 838 QNTANLGTGIIISLIYQWQLTLLALLAIVPIIATAGVVMKMLSGOALKDKKELEGAGKIA 897
QY 901 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITPFSFQAMMYSYAGCF 960
DB 898 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITPFSFQAMMYSYAGCF 957
QY 961 RFGAYLVAHLSMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVAAHIIIMIEKTP 1020
DB 958 RFGAYLVAHLSMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVAAHIIIMIEKTP 1017
QY 1021 IDSYSTEGLKNTLEGNVTFNEVFNPTRLDIPVLOGLSLEVKKGTALVGSSSGCGKS 1080

Db 298 SIGAPELLIYASALAFWYGTTLVLSGEYSIGQVLTVPFSSVLIGAFSVGQASPSIEAFAN 357
Qy 361 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
Db 358 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
Qy 421 QSGQTVALVNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 480
Db 418 QSGQTVALVNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 477
Qy 481 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 540
Db 478 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 537
Qy 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
Db 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
Qy 601 IAGFDDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSIDTLEMSSHD 660
Db 598 IAGFDDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSIDTLEMSSHD 657
Qy 661 SGSSLRKSTRSRVRSGQQRKLTKEALDESIPPVSWRIMKLNLTWPYFVVGVC 720
Db 658 SRSSLRKSTRSRVRSGQQRKLTKEALDESIPPVSWRIMKLNLTWPYFVVGVC 717
Qy 721 AIINGGLOPAFAVIFSKIIGITFRNDDAETKRONSLFSLFLVLGIVSFTTFLQGTTF 780
Db 718 AIINGGLOPAFAVIFSKIIGITFRNDDAETKRONSLFSLFLVLGIVSFTTFLQGTTF 777
Qy 781 GKAGEILTKELRYMVFESMLRODVSFDDPKNTTGALTTLANDAAOVKGAISRLAII 840
Db 778 GKAGEILTKELRYMVFESMLRODVSFDDPKNTTGALTTLANDAAOVKGAISRLAII 837
Qy 841 QNIANLGTGIIISLIYQWQTLTLLLAIVPIIAIAGVVMEMKLSQALDKKELEGAGKIA 900
Db 838 QNIANLGTGIIISLIYQWQTLTLLLAIVPIIAIAGVVMEMKLSQALDKKELEGAGKIA 897
Qy 901 TEAIENFRVTUSITOBOKFEMHYDQSLQVPRNSLRKAHIFGITFSTQAMVFSYAGCF 960
Db 898 TEAIENFRVTUSITOBOKFEMHYDQSLQVPRNSLRKAHIFGITFSTQAMVFSYAGCF 957
Qy 961 RFCAIYVAHLSMFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKYSAHHIMIEKTP 1020
Db 958 RFCAIYVAHLSMFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKYSAHHIMIEKTP 1017
Qy 1021 IDSISTEGLKPNTELEGNVTNEVFNYPTRLDIPVQLGSLVKKGOTLALVSSGCGKS 1080
Db 1018 IDSISTEGLKPNTELEGNVTNEVFNYPTRLDIPVQLGSLVKKGOTLALVSSGCGKS 1077
Qy 1081 TVVQLLERFYDPLAGKVLDDGKEIKOLNVQWMLRAHLGIVSQEPILFDCSISENAYGDNS 1140
Db 1078 TVVQLLERFYDPLAGKVLDDGKEIKOLNVQWMLRAHLGIVSQEPILFDCSISENAYGDNS 1137
Qy 1141 RVVSQEEIVRAAEKANHAFIESLPNKYSRFGDKGTQLSGGOKORIAIARALVRPHIL 1200
Db 1138 RVVSQEEIVRAAEKANHAFIESLPNKYSRFGDKGTQLSGGOKORIAIARALVRPHIL 1197
Qy 1201 LLDEATSAIDTSEKVVQEAALDKAREGRTTIVIAHRLSTTQONADLIIVFQNGRVKHEGTH 1260
Db 1198 LLDEATSAIDTSEKVVQEAALDKAREGRTTIVIAHRLSTTQONADLIIVFQNGRVKHEGTH 1257
Qy 1261 QLLAOKGIYFMSVSVQAGNRQ 1283
Db 1258 QLLAOKGIYFMSVSVQAGNRQ 1280

RESULT 12

US-09-584-586-4

Sequence 4, Application US/09584586

Patent No. 6933150

GENERAL INFORMATION:

Applicant: Sorrentino, Brian

; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
; US-09-584-586-4

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;

Best Local Similarity 96.4%; Pred. No. 0;

Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

Qy 1 MDLEGRNGGAENKPFKLNKSKDKKPKPTVSFMSFRYSNWLDKLYMVVGTAAII 60
Db 1 MDLEGRNGGAENKPFKLNKSKDKKPKPTVSFMSFRYSNWLDKLYMVVGTAAII 60
Qy 61 HGAGLPLMLLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAY 120
Db 61 HGAGLPLMLLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAY 117
Qy 121 YSGIGAGVLVAAYIQVSWFVCLAAGRQIHKIRKQFHAIMRQEIWFHVDHVGELNRLTD 180
Db 118 YSGIGAGVLVAAYIQVSWFVCLAAGRQIHKIRKQFHAIMRQEIWFHVDHVGELNRLTD 177
Qy 181 DYSKINEGIDKIGMEFQSMATFFTCFIVGFRGWLTLVILAIISVLGSAVWAKILS 240
Db 178 DYSKINEGIDKIGMEFQSMATFFTCFIVGFRGWLTLVILAIISVLGSAVWAKILS 237
Qy 241 SFTDKELLAYAKAGAVAEVLAARIVIAFGGOKKELERYNKNLEBAKIGIKKAITANI 300
Db 238 SFTDKELLAYAKAGAVAEVLAARIVIAFGGOKKELERYNKNLEBAKIGIKKAITANI 297
Qy 301 SIGAPELLIYASALAFWYGTTLVLSKEYSIGQVLTVPFSSVLIGAFSVGQASPSIEAFAN 360
Db 298 SIGAPELLIYASALAFWYGTTLVLSKEYSIGQVLTVPFSSVLIGAFSVGQASPSIEAFAN 357
Qy 361 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
Db 358 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
Qy 421 QSGQTVALVNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 480
Db 418 QSGQTVALVNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 477
Qy 481 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 540
Db 478 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 537
Qy 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
Db 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
Qy 601 IAGFDDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSIDTLEMSSHD 660
Db 598 IAGFDDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSIDTLEMSSHD 657
Qy 661 SGSSLRKSTRSRVRSGQQRKLTKEALDESIPPVSWRIMKLNLTWPYFVVGVC 720
Db 658 SRSSLRKSTRSRVRSGQQRKLTKEALDESIPPVSWRIMKLNLTWPYFVVGVC 717
Qy 721 AIINGGLOPAFAVIFSKIIGITFRNDDAETKRONSLFSLFLVLGIVSFTTFLQGTTF 780

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1021 Db      ||||| YSTEGMLPNTLEGNVTFGWVFNYPTRPDIPVLQGLSLEVKKGQTLALVSSCGGKSTVV 1080
1081 QY      ||||| QLLERFYDPLAGKVLLLDGKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENIAYGDNRSVV 1140
1081 Db      ||||| QLLERFYDPLAGKVLLLDGKEIKRLNVQWMLRAHLGIVSQEPILFDCSIAENIAYGDNRSVV 1140
1141 QY      ||||| SOEIVRAAKEANIHAFTESLPNKYSTRVGDGKTOLSGQOKORIAIARALVROPHTLLLD 1200
1141 Db      ||||| SOEIVRAAKEANIHAFTESLPNKYSTKVGDKGTOLSGQOKORIAIARALVROPHTLLLD 1200
1201 QY      ||||| EATSALDTESEKVOALDKAREGRTCIIVAHRLSTIONADLIVFONGRVKXEHGTHOOL 1260
1201 Db      ||||| EATSALDTESEKVOALDKAREGRTCIIVAHRLSTIONADLIVFONGRVKXEHGTHOOL 1260
1261 QY      ||||| LAQKGIYFSMVSVOAGAKRQ 1280
1261 Db      ||||| LAQKGIYFSMVSVOAGTKRQ 1280

RESULT 11
US-09-817-762-3
; Sequence 3, Application US/09817762
; Patent No. 6858774
; GENERAL INFORMATION:
; APPLICANT: Spalding, Edgar P.
; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 13238-00061
; CURRENT APPLICATION NUMBER: US/09/817,762
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/22363
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,814
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank P08183
; DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match          96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY      1 MDLEGRNGGASKNFFKLNKSKDKKERKPTVSVFSMFRYSNNWLDKLYMVVGTLLAAII 60
Db      1 MDLEGRNGGAKKQFFKLNKSEKDKKERKPTVSVFSMFRYSNNWLDKLYMVVGTLLAAII 60

QY      61 HGAGLPLMMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTPVFMNLEEDMTRYAYYSG 120
Db      61 HGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSNDINDTGFFMNLSEEDMTRYAYYSG 120

QY      121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKOPFHAIHQEIGHDFVDHVGELNTRLTDDVS 180
Db      121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKOPFHAIHQEIGHDFVDHVGELNTRLTDDVS 180

QY      181 KINEGIGDKIGMFFOSMATFFTFGTVFTRGKMLTLVILAISPVLCLSAAVWAKILSSFT 240
Db      181 KINEVIGDKIGMFFOSMATFFTFGTVFTRGKMLTLVILAISPVLCLSAAVWAKILSSFT 240

QY      241 DKELLAYAKAGAVEEVLAAIRTVIAFGCKKLELYRNKNLEAKRIGIKAITANISIG 300
Db      241 DKELLAYAKAGAVEEVLAAIRTVIAFGCKKLELYRNKNLEAKRIGIKAITANISIG 300

QY      301 AAFLLIYASYALAFWGTTLVLVSKEYSIGOVLTVFSSVLIGAFSVQASPSIEAFANARG 360

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301 AAFLLIYASALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGOQSPSIEAFANARG 360
361 AAFEIFKIIDNKPISDSYSGKHGPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
361 AAFEIFKIIDNKPISDSYSGKHGPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
421 QTVALVNSGCGKSTTVQMLQRLYDPTBGMVSVGDQIRTNVRLREIIGVVSQEPVLF 480
421 QTVALVNSGCGKSTTVQMLQRLYDPTBGMVSVGDQIRTNVRLREIIGVVSQEPVLF 480
481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
601 FDDGVIVEKGNHDELMEKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSG 660
601 FDDGVIVEKGNHDELMEKEGIYFKLVMTQTAGNEIELENAADESKSEIDALEMSSNDRS 660
661 SLIRKSTRSVRGSGQDRKSLSTKEALDESIIPVPSFWRIMKLNLTWPYFVGVFCALI 720
661 SLIRKSTRSVRGSGQDRKSLSTKEALDESIIPVPSFWRIMKLNLTWPYFVGVFCALI 720
721 NGGLQPAFAVIFSKIIGITFRNDADAETKRONSNLFSLLFLVLGIVSFTTFFLOGFTFGKA 780
721 NGGLQPAFAVIFSKIIGITFRNDADAETKRONSNLFSLLFLVLGIVSFTTFFLOGFTFGKA 780
781 GEILTKRLRYVFRSMLRQDVSFDDPKNTTGTALTRLANDAAVKGAIGSRLLAIITONI 840
781 GEILTKRLRYVFRSMLRQDVSFDDPKNTTGTALTRLANDAAVKGAIGSRLLAIITONI 840
841 ANLGTTIISLYGQWLTLLIIVPIITAIAGVEMKMLSGOALKOKKELSGAGKIA TEA 900
841 ANLGTTIISLYGQWLTLLIIVPIITAIAGVEMKMLSGOALKOKKELSGAGKIA TEA 900
901 IENFRVTVSLTQEQFHEMYAQSLOQVPYRNSLRKAHIFGIFTFTQAMMYFSYAGCPRFG 960
901 IENFRVTVSLTQEQFHEMYAQSLOQVPYRNSLRKAHIFGIFTFTQAMMYFSYAGCPRFG 960
961 AYLVAHLSMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVSAAHIMIEKTPLIDS 1020
961 AYLVAHLSMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVSAAHIMIEKTPLIDS 1020
1021 YSTGLKENTLEGNTVFNVEVFNPTPLDIIPVLOGLSLEVKKGOTLALVSGSGCGKSTVV 1080
1021 YSTGLKENTLEGNTVFNVEVFNPTPLDIIPVLOGLSLEVKKGOTLALVSGSGCGKSTVV 1080
1081 QLLERFYDPLAGKVLDDGKEIKOLNVQWLRHLGLVSOEPIIFDCSISENTAYGDSNRV 1140
1081 QLLERFYDPLAGKVLDDGKEIKOLNVQWLRHLGLVSOEPIIFDCSISENTAYGDSNRV 1140
1141 SOBEIVRAAKANTHAFTESLPNKYSTKTVGDKGTOLSGGQKORIAIARALVRQHILLD 1200
1141 SOBEIVRAAKANTHAFTESLPNKYSTKTVGDKGTOLSGGQKORIAIARALVRQHILLD 1200
1201 EATSALDTESEKVVQVQALDKAREGRTTIVIAHRLSTQNADLIIVFONGRVEKHTHQOL 1260
1201 EATSALDTESEKVVQVQALDKAREGRTTIVIAHRLSTQNADLIIVFONGRVEKHTHQOL 1260
1261 LAQKGIYFSMVSVQAGAKRQ 1280
1261 LAQKGIYFSMVSVQAGAKRQ 1280

RESULT 12

US-09-584-586-4
; Sequence 4, Application US/09584586
; Patent No: 6933150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian

; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
; US-09-584-586-4

Query Match 96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGRNGGAEGKKNFPLNNKSKKKKKKPTVSVFSPRYSNWLDKLYWVGTLLAAII 60
Db 1 MDLEGRNGGAEGKKNFPLNNKSKKKKKKPTVSVFSPRYSNWLDKLYWVGTLLAAII 60
Qy 61 HGAGLPLMLVFGDMTDTTPANAGNLGDLGALNNSSNITDTPVMNLEEDMTYAYVYSG 120
Db 61 HGAGLPLMLVFGDMTDTTPANAGNLGDLGALNNSSNITDTPVMNLEEDMTYAYVYSG 120
Qy 121 IGAGLVAAIYQVSWCLAAAGROIHKIRKQFFHAIHQEIGWDFDHDVDELNLTDDVS 180
Db 121 IGAGLVAAIYQVSWCLAAAGROIHKIRKQFFHAIHQEIGWDFDHDVDELNLTDDVS 180
Qy 181 KINEGIDGKIMGFQSMATPFTGFIIVGTRGWLTLVILAIISVPLGLSAVWAKILSSFT 240
Db 181 KINEGIDGKIMGFQSMATPFTGFIIVGTRGWLTLVILAIISVPLGLSAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAAVEEVLAAIRTVIAFGGOKKELERKNKLEAKRIGIKKAITANISIG 300
Db 241 DKELLAYAKAGAAVEEVLAAIRTVIAFGGOKKELERKNKLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASALAFWYGTTLVLSKEYSIGQVLTVFFSVLIGAFSVGOQSPSIEAFANARG 360
Db 301 AAFLLIYASALAFWYGTTLVLSKEYSIGQVLTVFFSVLIGAFSVGOQSPSIEAFANARG 360
Qy 361 AAFEIFKIIDNKPISDSYSGKHGPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
Db 361 AAFEIFKIIDNKPISDSYSGKHGPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
Qy 421 QTVALVNSGCGKSTTVQMLQRLYDPTBGMVSVGDQIRTNVRLREIIGVVSQEPVLF 480
Db 421 QTVALVNSGCGKSTTVQMLQRLYDPTBGMVSVGDQIRTNVRLREIIGVVSQEPVLF 480
Qy 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
Db 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
Qy 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Qy 601 FDDGVIVEKGNHDELMEKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSG 660
Db 601 FDDGVIVEKGNHDELMEKEGIYFKLVMTQTAGNEIELENAADESKSEIDALEMSSNDRS 660
Qy 661 SLIRKSTRSVRGSGQDRKSLSTKEALDESIIPVPSFWRIMKLNLTWPYFVGVFCALI 720
Db 661 SLIRKSTRSVRGSGQDRKSLSTKEALDESIIPVPSFWRIMKLNLTWPYFVGVFCALI 720
Qy 721 NGGLQPAFAVIFSKIIGITFRNDADAETKRONSNLFSLLFLVLGIVSFTTFFLOGFTFGKA 780

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721 NGGLQPAFAIFSKIIIGVTRIDDPETKQSNLFSLLFALGIISPIFFLQGFPGKA 780
781 GEILTKRLRYMVFRLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIITONI 840
781 GEILTKRLRYMVFRLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIITONI 840
781 GEILTKRLRYMVFRLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIITONI 840
841 ANLGTGIIISIIYQWLTLLALLAIVPIIAIAGVVMKMLSGOALKDKKLESGAGKIAEA 900
841 ANLGTGIIISIIYQWLTLLALLAIVPIIAIAGVVMKMLSGOALKDKKLESGAGKIAEA 900
901 IENERTVSLTOEQKFEHMYDOSLOVPRNSLRKAHIFGITTSFTQAMMYFSYACGRFFG 960
901 IENERTVSLTOEQKFEHMYDOSLOVPRNSLRKAHIFGITTSFTQAMMYFSYACGRFFG 960
961 AYLVAHSLMGFEDVLLVFSVAVFGAMAVGOVSSFAPDYAKAKVSAAHIMIEKTPILDS 1020
961 AYLVAHSLMGFEDVLLVFSVAVFGAMAVGOVSSFAPDYAKAKVSAAHIMIEKTPILDS 1020
1021 YSTEGLKPNTELEGNTVFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSSGCGKSTVV 1080
1021 YSTEGLKPNTELEGNTVFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSSGCGKSTVV 1080
1081 QLLERFYDPLAGKVLDDGKIKOLNVQWLRHAGIIVSOEPIFDCSISENIAIYCDNSRVV 1140
1081 QLLERFYDPLAGKVLDDGKIKOLNVQWLRHAGIIVSOEPIFDCSISENIAIYCDNSRVV 1140
1141 SOBEIVRAAKEANIHAFIESLPNKYSTRVCKGTQOLSGGQKORIAIARALVROPHILLD 1200
1141 SOBEIVRAAKEANIHAFIESLPNKYSTRVCKGTQOLSGGQKORIAIARALVROPHILLD 1200
1201 EATSALDTESEKVVQALDKAREGRICIVIAHRLSTIONADLIVFQNGRVEKHGTHOOL 1260
1201 EATSALDTESEKVVQALDKAREGRICIVIAHRLSTIONADLIVFQNGRVEKHGTHOOL 1260
1261 LAQKGIYFMSVVOAGAKRQ 1280
1261 LAQKGIYFMSVVOAGAKRQ 1280

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RESULT 13
US-08-583-276-19
; Sequence 19, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; APPLICANT: Tolstoshev, Paul
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DM4 V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712

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; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; US-08-583-276-19

Query Match      96.5%; Score 6206; DB 1; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGRNGAGAEKKNFKNKSKDKKPKPTVSFPMRYSNWLDKLYMVVGTLLAAII 60
DB 1 MDLEGRNGAGAEKKNFKNKSKDKKPKPTVSFPMRYSNWLDKLYMVVGTLLAAII 60
QY 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVKNLEEDMTYAYYS 120
DB 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVKNLEEDMTYAYYS 120
QY 121 ICAGVLVAAYIQVSWFCLAAAGRIHKKIRKOPFHAIMRQEIHFDFVHDVGEINLRLD 180
DB 121 ICAGVLVAAYIQVSWFCLAAAGRIHKKIRKOPFHAIMRQEIHFDFVHDVGEINLRLD 180
QY 181 KINEGIGDKIGMFOSMATFFTFIVGPTGRGKLTIVILAIISPVGLSAAVWAKILSPT 240
DB 181 KINEGIGDKIGMFOSMATFFTFIVGPTGRGKLTIVILAIISPVGLSAAVWAKILSPT 240
QY 241 DKELLAYAKAGAVEEVLAAITRTVIAFGQKKELRYNKNLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAVEEVLAAITRTVIAFGQKKELRYNKNLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASYALAFWYGTTLVLSEYSIGQVLTVPFSSVLIGAFSGVQASPSIEAFAN 360
DB 301 AAFLLIYASYALAFWYGTTLVLSEYSIGQVLTVPFSSVLIGAFSGVQASPSIEAFAN 360
QY 361 AAFEFKIIDNKPSIDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNKLK 420
DB 361 AAFEFKIIDNKPSIDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNKLK 420
QY 421 QTVALVGNSSGCGKSTTVQLMQRLYDPTGEMVSVGDQIRTNINVRFLRIIIGVSOE 480
DB 421 QTVALVGNSSGCGKSTTVQLMQRLYDPTGEMVSVGDQIRTNINVRFLRIIIGVSOE 480
QY 481 ATTIAENIRYGRQVNTMDEIEKAVKEANAYDFIMKLPKFDLTVGERGAQLSGGQK 540
DB 481 ATTIAENIRYGRQVNTMDEIEKAVKEANAYDFIMKLPKFDLTVGERGAQLSGGQK 540
QY 541 IARALVKNPKILLDEATSDALDTESEAVVQALDKARKGRITTVIAHRLSTVRNAD 600
DB 541 IARALVKNPKILLDEATSDALDTESEAVVQALDKARKGRITTVIAHRLSTVRNAD 600
QY 601 FDDGVIIVEKGNHDELMKEGIIYFKLVMTQTAGNEIELENAADSKSIDLTLEMS 660
DB 601 FDDGVIIVEKGNHDELMKEGIIYFKLVMTQTAGNEIELENAADSKSIDLTLEMS 660
QY 661 SLIRKSTRSVRGSGQDRKLTSTKALDESIPVSVFWRIMKLNLTWEPYFVGVFCAII 720
DB 661 SLIRKSTRSVRGSGQDRKLTSTKALDESIPVSVFWRIMKLNLTWEPYFVGVFCAII 720
QY 721 NGGLQPAFAIFSKIIIGVTRIDDPETKQSNLFSLLFALGIISPIFFLQGFPGKA 780
DB 721 NGGLQPAFAIFSKIIIGVTRIDDPETKQSNLFSLLFALGIISPIFFLQGFPGKA 780
QY 781 GEILTKRLRYMVFRLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIITONI 840
DB 781 GEILTKRLRYMVFRLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIITONI 840
QY 841 ANLGTGIIISIIYQWLTLLALLAIVPIIAIAGVVMKMLSGOALKDKKLESGAGKIAEA 900
DB 841 ANLGTGIIISIIYQWLTLLALLAIVPIIAIAGVVMKMLSGOALKDKKLESGAGKIAEA 900

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Db      841  ANLGTTGIIISFYGWOLTLTLLLAIVPIIAIAGVVMKMLSGQALKDKKKELEGAKIATEA  900
Qy      901  IENFRTVVSUTQEQKPEHMYDOSLOVYRNSLRKAHIFGTFSTQAMMYFSVAGCPRFG  960
Db      901  IENFRTVVSUTQEQKPEHMYAQSLOVYRNSLRKAHIFGTFSTQAMMYFSVAGCPRFG  960
Qy      961  AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPYAKAKVSAAHIMIEKTPLIDS  1020
Db      961  AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPYAKAKVSAAHIMIEKTPLIDS  1020
Qy     1021  YSTEGLPNTLEGNVTNEVFNPTRLDIPVQLGSLVKKGOTLALVSSGCGKSTVV  1080
Db     1021  YSTEGLPNTLEGNVTNEVFNPTRLDIPVQLGSLVKKGOTLALVSSGCGKSTVV  1080
Qy     1081  QLLERFYDPLAGKVLDDGKEIKOLNVQWLAHGIIVSQBPILFPCSIENIAYGDSRVV  1140
Db     1081  QLLERFYDPLAGKVLDDGKEIKOLNVQWLAHGIIVSQBPILFPCSIENIAYGDSRVV  1140
Qy     1141  SQBEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRPHILLD  1200
Db     1141  SQBEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRPHILLD  1200
Qy     1201  EATSALDTESEKVVQBALDKAREGRTCVIAHRLSTTIONADLIIVFONGRVEKHGTHQOL  1260
Db     1201  EATSALDTESEKVVQBALDKAREGRTCVIAHRLSTTIONADLIIVFONGRVEKHGTHQOL  1260
Qy     1261  LAQGIYFSMVSVQAGAKRQ  1280
Db     1261  LAQGIYFSMVSVQAGAKRQ  1280

RESULT 14
5206352-4
; Patient No. 5206352
; Applicant: Robinson, Igor B.; Pastan Ira H.; Gottesman,
; Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/622,836
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO: 4
; LENGTH: 1280
5206352-4

Query Match      96.6%; Score 6206; DB 7; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Qy      1  MDLEGGDRNGAEKKNFFKLNKSKDKKERKPTVSVFSMFYSYNWLDKLYVMVGTAAII  60
Db      1  MDLEGGDRNGGAKKNFFKLNKSKDKKERKPTVSVFSMFYSYNWLDKLYVMVGTAAII  60
Qy     61  HGAGLPLMLVFGDMTDTFANAGNLGDI/GALLTNSNITDTPVPMNLFEEDMTRVAYYSG  120
Db     61  HGAGLPLMLVFGDMTDTFANAGNLGDI/GALLTNSNITDTPVPMNLFEEDMTRVAYYSG  120
Qy     121  IGAGVLVAAYIQVSWFCLAAQROIHKIRKQPFHMRQEIQGFVDVHVGELNLTDDVS  180
Db     121  IGAGVLVAAYIQVSWFCLAAQROIHKIRKQPFHMRQEIQGFVDVHVGELNLTDDVS  180
Qy     181  KINGIGDKIGMPTQSMATFTFTGIVGTRGKMLTLVLAISPVGLSAAVWAKILSFT  240
Db     181  KINGIVGDKIGMPTQSMATFTFTGIVGTRGKMLTLVLAISPVGLSAAVWAKILSFT  240
Qy     241  DKELLAYAKAGAAEVLAAIRTVIAFGGQKKELEKRYNKNLEAKRIGIKKAITANISIG  300

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QY 1 MDLEGRNGAEKKNFKLANKSKDKKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEKKNFKLANKSKDKKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALL--TNSNITDTVPVNNLEEDMTYAY 117
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTVPVNNLEEDMTYAY 120
QY 118 YSGIGAGVLVAAYIQVSWFCLAAAGROIHKIRKQFFHAIMROEIGWFDVHDVGBELNRLTD 177
DB 121 YSGIGAGVLVAAYIQVSWFCLAAAGROIHKIRKQFFHAIMROEIGWFDVHDVGBELNRLTD 180
QY 178 DYSKINEGIDKLGMPFQSMATFTFGIVGFTGKWLTLVILAI SPVLGLSAAVAKILS 237
DB 181 DYSKINEGIDKLGMPFQSMATFTFGIVGFTGKWLTLVILAI SPVLGLSAAVAKILS 240
QY 238 SFTDKELLAYAKAGAVAEVLAARTVIAFGGOKKELERNYNNLEAKRIGIKKAITANI 297
DB 241 SFTDKELLAYAKAGAVAEVLAARTVIAFGGOKKELERNYNNLEAKRIGIKKAITANI 300
QY 298 SIGAAFLIIYASVALAFWYGTTLVLKEYSIGOVLTVPFVSVLIGAFVGOASPISAFAN 357
DB 301 SIGAAFLIIYASVALAFWYGTTLVLKEYSIGOVLTVPFVSVLIGAFVGOASPISAFAN 360
QY 358 ARGAAPFIIKIDNKPSIDSYSGKHGPDNIKGNLERNVHFSYPSRKEVKILKGLNLY 417
DB 361 ARGAAPFIIKIDNKPSIDSYSGKHGPDNIKGNLERNVHFSYPSRKEVKILKGLNLY 420
QY 418 QSGQTTVALVNSGCGSKTTVQLMORLYDPTGEMVSDGQDIRTNVFLREIIGVVSQEP 477
DB 421 QSGQTTVALVNSGCGSKTTVQLMORLYDPTGEMVSDGQDIRTNVFLREIIGVVSQEP 480
QY 478 VLFATTIAENIRYGREVDVTMDEIEKAVKEANAYDFIMKLPQKEDTLVGERGAOLSGQKQ 537
DB 481 VLFATTIAENIRYGREVDVTMDEIEKAVKEANAYDFIMKLPQKEDTLVGERGAOLSGQKQ 540
QY 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
DB 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
QY 598 IAGFDGVIYKGNHDELMKEGIIYFKLVTMGTAGNIELENAADBSKSIDTLEMSHD 657
DB 601 IAGFDGVIYKGNHDELMKEGIIYFKLVTMGTAGNIELENAADBSKSIDTLEMSHD 660
QY 658 SGSSLRKRSTRSVRSGQDRKLSYKEALDESIPVSPWRIMKLNLTWPYFVVGVC 717
DB 661 SGSSLRKRSTRSVRSGQDRKLSYKEALDESIPVSPWRIMKLNLTWPYFVVGVC 720
QY 718 AITNGLOPAFAVIFSKIIIGIFTRNDAAETKRONSLFSLFLVLGIVSFITPFLQGTF 777
DB 721 AITNGLOPAFAVIFSKIIIGIFTRNDAAETKRONSLFSLFLVLGIVSFITPFLQGTF 780
QY 778 GKAGEILTKELRYVWFMSLRQDVSWFDDPKNTGTALTRLANDAAOVKAIGSLRLAIT 837
DB 781 GKAGEILTKELRYVWFMSLRQDVSWFDDPKNTGTALTRLANDAAOVKAIGSLRLAIT 840
QY 838 QNTANLGTGIIISLIYQWQLTLLLAIVPIIAGVVMKLSQALDKKKELEGAKIA 897
DB 841 QNTANLGTGIIISLIYQWQLTLLLAIVPIIAGVVMKLSQALDKKKELEGAKIA 900
QY 898 TEAIENFRVTSITQEQFHEMYDQSLQVPRNSLRKAHIFGITFSQAMTFYSYAGCP 957
DB 901 TEAIENFRVTSITQEQFHEMYDQSLQVPRNSLRKAHIFGITFSQAMTFYSYAGCF 960
QY 958 RFCAYLVAHSLMFEDVLLVPSAVVFCAMAVGVSSFPADYAKAKVSAAHIMIEKTPL 1017
DB 961 RFCAYLVAHSLMFEDVLLVPSAVVFCAMAVGVSSFPADYAKAKVSAAHIMIEKTPL 1020
QY 1018 IDSYSYEGKLPNTLEGNTVNEVFNPTRIDIPVLOGLSLVKKGTGTALVSGSGGCKS 1077
DB 1021 IDSYSYEGKLPNTLEGNTVNEVFNPTRIDIPVLOGLSLVKKGTGTALVSGSGGCKS 1080
QY 1078 TVVQLLERYFDPLAGKVLDDGKEIKQLNVQWLAHGLGIVSQEPILFDCSISENIAVGDNS 1137

DB 1081 TVVQLLERYFDPLAGKVLDDGKEIKQLNVQWLAHGLGIVSQEPILFDCSISENIAVGDNS 1140
QY 1138 RVVSQEBIVRAAKEANIHAIESLPNKYSTRVGDKGTQSGGOKORAIARALVRPHIL 1197
DB 1141 RVVSQEBIVRAAKEANIHAIESLPNKYSTRVGDKGTQSGGOKORAIARALVRPHIL 1200
QY 1198 LIDEATSAIDTSEKVVQVQALDKAREGRTCIIVIAHRLSTIQNADLLVFPONGRVKHEGTH 1257
DB 1201 LIDEATSAIDTSEKVVQVQALDKAREGRTCIIVIAHRLSTIQNADLLVFPONGRVKHEGTH 1260
QY 1258 QOLLAOKGIYFMSVSVQAGAKRQ 1280
DB 1261 QOLLAOKGIYFMSVSVQAGAKRQ 1283

RESULT 6
US-09-584-586-2
Sequence 2, Application US/09584586
Patent No. 6933130
GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Bunting, Kevin
TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
FILE REFERENCE: 1340-1-021CIP
CURRENT APPLICATION NUMBER: US/09/584,586
CURRENT FILING DATE: 2000-05-31
EARLIER APPLICATION NUMBER: US 60/086,988
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: PCT/US99/11825
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human MDR 185-G
US-09-584-586-2

Query Match 96.8%; Score 6218; DB 2; Length 1280;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 1237; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEKKNFKLANKSKDKKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEKKNFKLANKSKDKKERTVSVFMSFRYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNNLEEDMTYAYYSG 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNNLEEDMTYAYYSG 120
QY 121 IGAGLVAAVYIQVSWFCLAAAGROIHKIRKQFFHAIMROEIGWFDVHDVGBELNRLTDVVS 180
DB 121 IGAGLVAAVYIQVSWFCLAAAGROIHKIRKQFFHAIMROEIGWFDVHDVGBELNRLTDVVS 180
QY 181 KINEGIDKLGMPFQSMATFTFGIVGFTGKWLTLVILAI SPVLGLSAAVAKILSSFT 240
DB 181 KINEGIDKLGMPFQSMATFTFGIVGFTGKWLTLVILAI SPVLGLSAAVAKILSSFT 240
QY 241 DKELLAYAKAGAVAEVLAARTVIAFGGOKKELERNYNNLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAVAEVLAARTVIAFGGOKKELERNYNNLEAKRIGIKKAITANISIG 300
QY 301 AAPLLIYASVALAFWYGTTLVLKEYSIGOVLTVPFVSVLIGAFVGOASPISAFANARG 360
DB 301 AAPLLIYASVALAFWYGTTLVLKEYSIGOVLTVPFVSVLIGAFVGOASPISAFANARG 360
QY 361 AAPFEIKIDNKPSIDSYSGKHGPDNIKGNLERNVHFSYPSRKEVKILKGLNLYVQSG 420
DB 361 AAPFEIKIDNKPSIDSYSGKHGPDNIKGNLERNVHFSYPSRKEVKILKGLNLYVQSG 420

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QY 421 QTVALVNSGCGKSTTVOLMORLYDTEGMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
DB 421 QTVALVNSGCGKSTTVOLMORLYDTEGMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
QY 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGRGAQLSGGQKORIA 540
DB 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGRGAQLSGGQKORIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDSGS 660
DB 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDSGS 660
QY 661 SLIRKSTRSRVSGSQODRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCALI 720
DB 661 SLIRKSTRSRVSGSQODRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCALI 720
QY 721 NGGLQAPAFIVFSKIIGIFTRNDADTKRQNSNLFSLFLVLGIVSFTFFLQGTFFGKA 780
DB 721 NGGLQAPAFIVFSKIIGIFTRNDADTKRQNSNLFSLFLVLGIVSFTFFLQGTFFGKA 780
QY 781 GEILTKRLRYMYFRSMRLQDVSFDDPKNTTGTALTRLANDAAOVKGAIGSLAIITONI 840
DB 781 GEILTKRLRYMYFRSMRLQDVSFDDPKNTTGTALTRLANDAAOVKGAIGSLAIITONI 840
QY 841 ANLGTGIIISLYGQWLTLLMIAIPIIAIAGVEMKMLSGQALDKKKELEGAGKIATEA 900
DB 841 ANLGTGIIISLYGQWLTLLMIAIPIIAIAGVEMKMLSGQALDKKKELEGAGKIATEA 900
QY 901 IENFTVSVLTOEQKFEHMYDOSLOVPYRNSLRKAHIFGITPSFTQAMMYFSYACGFRFG 960
DB 901 IENFTVSVLTOEQKFEHMYDOSLOVPYRNSLRKAHIFGITPSFTQAMMYFSYACGFRFG 960
QY 961 AYLVASHMSFEDVLLVFSNAVFGAMVGVSSPAPDYAKAKVSAHAHIMIEKTPILDS 1020
DB 961 AYLVASHMSFEDVLLVFSNAVFGAMVGVSSPAPDYAKAKVSAHAHIMIEKTPILDS 1020
QY 1021 YSTGLKENTLEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSGSGCKSTV 1080
DB 1021 YSTGLKENTLEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSGSGCKSTV 1080
QY 1081 QLLERFYDPLAGKVLDDGKEIKOLNVQMLRAHLGIVSQEPILFDCSISENIAYGNSRV 1140
DB 1081 QLLERFYDPLAGKVLDDGKEIKOLNVQMLRAHLGIVSQEPILFDCSISENIAYGNSRV 1140
QY 1141 SQEEIVRAAKENIHAFTESLBNKYSTRVGDGKTLGSGGQKORIAIARALVRQPHILLD 1200
DB 1141 SQEEIVRAAKENIHAFTESLBNKYSTRVGDGKTLGSGGQKORIAIARALVRQPHILLD 1200
QY 1201 EATSDALDTESEKVOEALDKAREGRTTIVIAHRLSTIONADLIIVFQNGRVRKEHGTTHOOL 1260
DB 1201 EATSDALDTESEKVOEALDKAREGRTTIVIAHRLSTIONADLIIVFQNGRVRKEHGTTHOOL 1260
QY 1261 LAQKGIYFSMVSVQAGKRRQ 1280
DB 1261 LAQKGIYFSMVSVQAGKRRQ 1280

```

RESULT 7
 US-09-767-594-2
 ; Sequence 2, Application US/09767594
 ; Patent No. 6521635
 ; GENERAL INFORMATION:
 ; APPLICANT: Bates, Susan
 ; APPLICANT: Robey, Robert
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

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; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2

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Query Match          96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGDRNGGAEKKNFFKLNKSKDKKERKPTVSFVSMFYSNWLDKLYMVVGTLLAII 60
DB 1 MDLEGDRNGGAEKKNFFKLNKSKDKKERKPTVSFVSMFYSNWLDKLYMVVGTLLAII 60
QY 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVNNLEEDMTRVAYYS 120
DB 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVNNLEEDMTRVAYYS 120
QY 121 IGAGVLAAYIQVSWFCLAAAGROHKIRKQFFHAIHQEIGWFDVHVGELNLTDDVS 180
DB 121 IGAGVLAAYIQVSWFCLAAAGROHKIRKQFFHAIHQEIGWFDVHVGELNLTDDVS 180
QY 181 KINEGIGDKIGMFFQSMATFTGTVGTRGWKLTLLVLAISPVGLSAAVWAKILSFT 240
DB 181 KINEGIGDKIGMFFQSMATFTGTVGTRGWKLTLLVLAISPVGLSAAVWAKILSFT 240
QY 241 DKELLAYAKAGAAVEVLAAIRTVIAFGGQKELERYNNKLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAAVEVLAAIRTVIAFGGQKELERYNNKLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASVALAPWYGTTLVLSKEYSIGVLTVPFVSVLGAQSVGOASPIEFANARG 360
DB 301 AAFLLIYASVALAPWYGTTLVLSKEYSIGVLTVPFVSVLGAQSVGOASPIEFANARG 360
QY 361 AAFEIFKIIDNKPSIDSYSGSKGHPDNIKGNLFRNVHFSYPSRKEVKILKGLNLYQSG 420
DB 361 AAFEIFKIIDNKPSIDSYSGSKGHPDNIKGNLFRNVHFSYPSRKEVKILKGLNLYQSG 420
QY 421 QTVALVNSGCGKSTTVOLMORLYDTEGMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
DB 421 QTVALVNSGCGKSTTVOLMORLYDTEGMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
QY 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGRGAQLSGGQKORIA 540
DB 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGRGAQLSGGQKORIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDSGS 660
DB 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDSGS 660
QY 661 SLIRKSTRSRVSGSQODRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCALI 720
DB 661 SLIRKSTRSRVSGSQODRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCALI 720
QY 721 NGGLQAPAFIVFSKIIGIFTRNDADTKRQNSNLFSLFLVLGIVSFTFFLQGTFFGKA 780
DB 721 NGGLQAPAFIVFSKIIGIFTRNDADTKRQNSNLFSLFLVLGIVSFTFFLQGTFFGKA 780

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QY 1141 SOEIVRAAKENIAHAFIESLPNKYSTKVGDKGTOLSGQKORIAIARALVROPHILLD 1200
DB 1141 SOEIVRAAKENIAHAFIESLPNKYSTKVGDKGTOLSGQKORIAIARALVROPHILLD 1200
QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNALDIVVFQNGRVEKHTHQOL 1260
DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNALDIVVFQNGRVEKHTHQOL 1260
QY 1261 LAOKGIYFMSVVOAGTKRQ 1280
DB 1261 LAOKGIYFMSVVOAGTKRQ 1280

RESULT 4
US-10-101-433A-5
; Sequence 5, Application US/10101433A
; Patent No. 685812
; GENERAL INFORMATION:
; APPLICANT: Hanscom, Sara
; APPLICANT: Crepi, Charles
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307/70019
; CURRENT APPLICATION NUMBER: US/10/101,433A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/277,095
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-433A-5

Query Match 100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGAKKKNFFKLNKSEKDKKPKTQVSVFMSFRYSNWLDKLYMVGTLAAII 60
DB 1 MDLEGRNGAKKKNFFKLNKSEKDKKPKTQVSVFMSFRYSNWLDKLYMVGTLAAII 60
QY 61 HGAGLPLMLVCEMTDIFANAGNLEDLMSNITNRSNDINDTGFPMNLEEDMTYAYYSG 120
DB 61 HGAGLPLMLVCEMTDIFANAGNLEDLMSNITNRSNDINDTGFPMNLEEDMTYAYYSG 120
QY 121 IGAGVLVAAYIOVSFWCLAGRQIHKIRKQFPHAIMRQSIGWFDVHVGELNRLTDDVS 180
DB 121 IGAGVLVAAYIOVSFWCLAGRQIHKIRKQFPHAIMRQSIGWFDVHVGELNRLTDDVS 180
QY 181 KINEVIGDKIGMFFOSMATFTFTGIVGTRGKLTILAILSPVLGSLNAAVWAKILSFT 240
DB 181 KINEVIGDKIGMFFOSMATFTFTGIVGTRGKLTILAILSPVLGSLNAAVWAKILSFT 240
QY 241 DKELLAYAKAGAAVEVLAAITRTVAFGGQKELERYNKLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAAVEVLAAITRTVAFGGQKELERYNKLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASALAFWYGTTLVLSEYSIGOVLTFFSVLIGAFVQASPSIEAFANARG 360
DB 301 AAFLLIYASALAFWYGTTLVLSEYSIGOVLTFFSVLIGAFVQASPSIEAFANARG 360
QY 361 AAYEIFKIIDNKPSIDSYSGSKHPDNIKNLEPRNVHFSVPSRKEVKILKGLNKLKVSQ 420
DB 361 AAYEIFKIIDNKPSIDSYSGSKHPDNIKNLEPRNVHFSVPSRKEVKILKGLNKLKVSQ 420
QY 421 QVALVNSCGGKSTTVLMQRLYDPTGEMVSDGDIRTNVRLREIIGVVSQBPVL 480
DB 421 QVALVNSCGGKSTTVLMQRLYDPTGEMVSDGDIRTNVRLREIIGVVSQBPVL 480
QY 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKORIA 540
DB 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKORIA 540

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RESULT 5
 US-09-817-762-3
 ; Sequence 3, Application US/09817762
 ; Patent No. 6858774
 ; GENERAL INFORMATION:
 ; APPLICANT: Spalding, Edgar P.
 ; APPLICANT: No. 6858774, Bosl
 ; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 13238-00061
 ; CURRENT APPLICATION NUMBER: US/09/817,762
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: PCT/US99/22363
 ; PRIOR FILING DATE: 1999-09-24
 ; PRIOR APPLICATION NUMBER: US 60/101,814
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSeq for Windows Version 4.0

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DB 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKORIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDCGVIVKGNHDELMEKEGIYFKLVTMOTAGNEVELENAADESKSEIDALEMSSNDSRS 660
DB 601 FDCGVIVKGNHDELMEKEGIYFKLVTMOTAGNEVELENAADESKSEIDALEMSSNDSRS 660
QY 661 SLIRKSTRSVRGSAQDRKLSKEALDESPVPSFWIRIMKLNLTENFYFVGVFCALII 720
DB 661 SLIRKSTRSVRGSAQDRKLSKEALDESPVPSFWIRIMKLNLTENFYFVGVFCALII 720
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DB 721 NGLOPAPAFIIFSKIIIGVFTTRIDDPETKRONSLFSLFLALGIISFIFFLQGTGKA 780
QY 781 GEILTTLRLYVMFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSRLAVITQNI 840
DB 781 GEILTTLRLYVMFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSRLAVITQNI 840
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DB 841 ANLGTGIIISFIYQWQLTLLAILAIVPIIAIAGVVMKMLSCOALKDKKELEGAGKIA TEA 900
QY 901 IENPRTVVSITOBQKFEHMYAQSLQVPRNSLRKAHIFGITFTFOAMVPSYAGCFRFG 960
DB 901 IENPRTVVSITOBQKFEHMYAQSLQVPRNSLRKAHIFGITFTFOAMVPSYAGCFRFG 960
QY 961 AYLVAHKLMSFEDVLLVFSAVVFGMAVGOVVSFADPYAKAKISAAHIIIMEKTEPLIDS 1020
DB 961 AYLVAHKLMSFEDVLLVFSAVVFGMAVGOVVSFADPYAKAKISAAHIIIMEKTEPLIDS 1020
QY 1021 YSTEGLMPTNLEGNVTFGEVFNYPTRPDIPVLQGLSEVKKGTOLALVSSGCGKSTVV 1080
DB 1021 YSTEGLMPTNLEGNVTFGEVFNYPTRPDIPVLQGLSEVKKGTOLALVSSGCGKSTVV 1080
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DB 1081 QLLERPYDPLACKVLLDGEIKRLNVQMLRAHLGIVSQEPILFDCSIAENIAYGNSRVV 1140
QY 1141 SOEIVRAAKENIAHAFIESLPNKYSTKVGDKGTOLSGQKORIAIARALVROPHILLD 1200
DB 1141 SOEIVRAAKENIAHAFIESLPNKYSTKVGDKGTOLSGQKORIAIARALVROPHILLD 1200
QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNALDIVVFQNGRVEKHTHQOL 1260
DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNALDIVVFQNGRVEKHTHQOL 1260
QY 1261 LAOKGIYFMSVVOAGTKRQ 1280
DB 1261 LAOKGIYFMSVVOAGTKRQ 1280

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; SEQ ID NO 3
; LENGTH: 1280
; TYPE: PR
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank P08183
; DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match 100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLEGRNGGAKKQFFLNKSEKDKKPKTVSVFMSFRYSNWLKLYVMVGTAAII 60
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Db 181 KINEVIGDKIGMFFOSMAFTFTGPIVGTGRGKLTIVILASPVGLSAAVWAKILSFT 240
Qy 241 DKELAYAKAGAEVLAARTVIAFGGKKELRYNKNLEAKRIGIKKAITANISIG 300
Db 241 DKELAYAKAGAEVLAARTVIAFGGKKELRYNKNLEAKRIGIKKAITANISIG 300
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Db 301 AAFLLIYASALAFWGTTLVLSGYSISGVLTVPFVSVLIGAFSVQASPSIEAFANARG 360
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Db 361 AAYEFKIIDNKPSIDTSKSGHKPDNKGNEFNHVSFSPSRKEVILKGLNKLKVGSG 420
Qy 421 QTVALVNGSGCGKSTTVLMQRLYDPTGMSVSDQDRTINVRFLRIIIGVSEPVLF 480
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Db 781 GEILTTELRYMVFRSMRLQDVSFDDPKNTTGALTTRLANDAAQVKGAGISRLAVITQNI 840
Qy 841 ANLGTGIIISFIYQWQTLTLLLAIVPIIAIAGVEMKMLSGOALKDKKELEGACKIATEA 900
Db 841 ANLGTGIIISFIYQWQTLTLLLAIVPIIAIAGVEMKMLSGOALKDKKELEGACKIATEA 900

RESULT 6
US-09-584-586-4
; Sequence 4, Application US/09584586
; Patent No. 6933150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584, 586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086, 988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
US-09-584-586-4

Query Match 100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLEGRNGGAKKQFFLNKSEKDKKPKTVSVFMSFRYSNWLKLYVMVGTAAII 60
Db 1 MDLEGRNGGAKKQFFLNKSEKDKKPKTVSVFMSFRYSNWLKLYVMVGTAAII 60
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Db 181 KINEVIGDKIGMFFOSMAFTFTGPIVGTGRGKLTIVILASPVGLSAAVWAKILSFT 240
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Db 361 AAYEFKIIDNKPSIDTSKSGHKPDNKGNEFNHVSFSPSRKEVILKGLNKLKVGSG 420
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Db 421 QTVALVNGSGCGKSTTVLMQRLYDPTGMSVSDQDRTINVRFLRIIIGVSEPVLF 480
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Db 481 ATTIAENIRYGRNVTWDEIEKAVKANAYDFIMKLPKFDLTVGERGAQLSGGQKRIA 540
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Qy 601 FDDGVIVEKGNHDELMKEGIFKLVMTQAGNEVELENADESKSEIDALEMSNDRS 660
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Db 721 NGLOPAFAIFSKIIGVTRIDDPETKRONSLFSLFLALGIIISFITPLOGFTFGKA 780
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Db 781 GEILTKELRYVPSMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSLRAVITONI 840
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Db 1201 EATSALDTESEKVVQEAALDKAREGRTCIVIAHRLSTIQNADLIIVFONGRKEHGHQOL 1260
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Db 1261 LAQKGIYFMSVSVQAGTKRQ 1280

RESULT 7
US-08-583-276-19
; Sequence 19, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; APPLICANT: Tolstoshev, Paul
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712
; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
US-08-583-276-19

Query Match 99.9%; Score 6428; DB 1; Length 1280;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLEGDRNGGAKGNFFKLNKSEKDKKPKTVSVFSMFRYSNMLDKLYMVVGTLLAAII 60
Db 1 MLEGDRNGGAKGNFFKLNKSEKDKKPKTVSVFSMFRYSNMLDKLYMVVGTLLAAII 60
Qy 61 HGAGLPLMLVFGEMTDIFANAGNLEDMSNTNRSDINDTGFNMLEDMDTRYAYYSG 120
Db 61 HGAGLPLMLVFGEMTDIFANAGNLEDMSNTNRSDINDTGFNMLEDMDTRYAYYSG 120
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Db 181 KINEVIGDKIGMFFQSMATFTGFTVGTGKGLTLVLAISPVGLSAAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAAVEVLAAITRTVAFGGOKKELRYNKNLEBAKRGIGIKKAITANISIG 300
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Db 301 AAFLLIYASYALAFWYGTTLVLGSGYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360

Db 418 QSGQTVLVGNCGCKSTTVQLMORLYDPTBGMVSDGQDIRTINVRFLRIIGVVSQEP 477
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Db 538 RIAIARALVRNPKILLDEATSAIDTESAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
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Db 718 AINGGLQPAFAVIFSKIIIGIFTRNDDAETKQNSNLSFLFLVLGIVSFITFFLQGPFF 777
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Db 1258 QOLLAQKGIYFSMVSQVQAKRQ 1280

RESULT 5

ID MDRI HUMAN STANDARD. PRT: 1280 AA.
AC P08183; Q12755; Q14872;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006, entry version 2.
DT 07-MAR-2006, entry version 78.
DE Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen).
GN Name=ABCB1; Synonyms=MDR1, PGP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT VAL-185.
RX MEDLINE=87028230; PubMed=2876781; DOI=10.1016/0092-8674(86)90595-7;
RA Chen C.-J., Chin J.E., Ueda K., Clark D.P., Pastan I., Gottesman M.M.,
RA Roninson I.B.;
RT "Internal duplication and homology with bacterial transport proteins
in the mdr1 (P-glycoprotein) gene from multidrug-resistant human
cells.";
RL Cell 47:381-389 (1986).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90094448; PubMed=1967175;
RA Chen C.-J., Clark D.P., Ueda K., Pastan I., Gottesman M.M.,
RA Roninson I.B.;
RT "Genomic organization of the human multidrug resistance (MDR1) gene
and origin of P-glycoproteins.";
RL J. Biol. Chem. 265:506-514 (1990).
[3]
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT VAL-185.
RX MEDLINE=97190336; PubMed=9038218; DOI=10.1074/jbc.272.9.5413;
RA Chen G., Duran G.E., Steger K.A., Lacayo N.J., Jaffrezou J.P.,
RA Dumontet C., Sikic B.I.;
RT "Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein,
altered phenotype, and resistance to cyclosporins.";
RL J. Biol. Chem. 272:5974-5982 (1997).
[4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LEU-17; ASP-21;
RX MEDLINE=400; LYS-566; CYS-593; VAL-836; ALA-1051; THR-1141 AND ILE-1251.
RA Livingston R.J., Rieder N., Rajkumar N., Downing T.K., Olson A.N.,
RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
RA Swanson J.E., McFarland I., Tool B., Park C., Nickerson D.A.;
RT "NTEHS-SNPs, environmental genome project, NIEHS ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fowell G.A., Delehaanty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vazbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfs T., Rock S.M.,
RA Tin-Wellam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubbs K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Pury T.S.,
RA Baertsch R.A., Brent M.E., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
[6]
RP NUCLEOTIDE SEQUENCE OF 178-215 AND 800-856.
RX MEDLINE=90290529; PubMed=1972623;
RA Gekeler V., Weger S., Probst H.;
RT "mdr1/P-glycoprotein gene segments analyzed from various human
leukemic cell lines exhibiting different multidrug resistance
profiles.";
RL Biochem. Biophys. Res. Commun. 169:796-802 (1990).
[7]
RP NUCLEOTIDE SEQUENCE OF 1-23, AND VARIANT SER-893.
RX MEDLINE=89322246; PubMed=2568932;
RA Kioka N., Tsubota J., Kakehi Y., Komano T., Gottesman M.M., Pastan I.,
RA Ueda K.;

"P-glycoprotein gene (MDR1) cDNA from human adrenal: normal P-glycoprotein carries Gly185 with an altered pattern of multidrug resistance." *Biochem. Biophys. Res. Commun.* 162:224-231 (1989).

[8]

RP MEDLINE=21156763; PubMed=11258197; DOI=10.1517/14622416.2.1.51; Kerb R., Hofmeyer S., Brinkmann U., "ABC drug transporters: hereditary polymorphisms and pharmacological impact in MDR1, MRP1 and MRP2." *Pharmacogenomics* 2:51-64 (2001).

[9]

RP VARIANT VAL-185.

RP MEDLINE=88223345; PubMed=2897240; Choi K.H., Chen C.-J., Kriegler M., Roninson I.B.; "An altered pattern of cross-resistance in multidrug-resistant human cells results from spontaneous mutations in the mdr1 (P-glycoprotein) gene." *Cell* 53:519-529 (1988).

[10]

RP VARIANTS SER-893 AND THR-999.

RP MEDLINE=98139471; PubMed=9473242; Mickley L.A., Lee J.-S., Weng Z., Zhan Z., Alvarez M., Wilson W., Bates S.E., Fojo T.; "Genetic polymorphism in MDR-1: a tool for examining allelic expression in normal cells, unselected and drug-selected cell lines, and human tumors." *Blood* 91:1749-1756 (1998).

[11]

RP VARIANT ASP-21.

RP MEDLINE=20251368; PubMed=10790226; DOI=10.1002/(SICI)1098-1004(200005)15:5<486::AID-HUMU26>3.3.CO;2-G; Declèves X., Chevillard S., Charpentier C., Vielh P., Laplanche J.L.; "A new polymorphism (N21D) in the exon 2 of the human MDR1 gene encoding the P-glycoprotein." *Hum. Mutat.* 15:486-486 (2000).

[12]

RP VARIANTS ASP-21; LEU-103 AND ASN-400.

RP MEDLINE=20202660; PubMed=10716719; DOI=10.1073/pnas.050585397; Hoffmeyer S., Burk O., von Richter O., Arnold H.P., Brockmøller J., John A., Cascorbi I., Gerloff T., Roots I., Eichelbaum M., Brinkmann U.; "Functional polymorphisms of the human multidrug-resistance gene: multiple sequence variations and correlation of one allele with P-glycoprotein expression and activity in vivo." *Proc. Natl. Acad. Sci. U.S.A.* 97:3473-3478 (2000).

[13]

RP VARIANTS ASP-21; ASN-400; SER-893; THR-893 AND PRO-1107.

RP MEDLINE=21135363; PubMed=11240981; DOI=10.1067/mcp.2001.114164; Cascorbi I., Gerloff T., John A., Meisel C., Hofmeyer S., Schwab M., Schaeffeler E., Eichelbaum M., Brinkmann U., Roots I.; "Frequency of single nucleotide polymorphisms in the P-glycoprotein drug transporter MDR1 gene in white subjects." *Clin. Pharmacol. Ther.* 69:169-174 (2001).

[14]

RP VARIANT LYS-108.

RP PubMed=15618700; DOI=10.2133/dmpk.17.479; Honda T., Dan Y., Koyabu N., Ieiri I., Otsubo K., Higuchi S., Ohtani H., Sawada J.; "Polymorphism of MDR1 gene in healthy Japanese subjects: a novel SNP with an amino acid substitution (Glu108Lys)." *Drug Metab. Pharmacokinet.* 17:479-481 (2002).

[15]

RP VARIANT ILE-1251.

RP PubMed=15618713; DOI=10.2133/dmpk.17.566; Itoda M., Saito Y., Komamura K., Ueno K., Kamakura S., Ozawa S., Sawada J.; "Twelve novel single nucleotide polymorphisms in ABCB1/MDR1 among Japanese patients with ventricular tachycardia who were administered amiodarone." *Drug Metab. Pharmacokinet.* 17:566-571 (2002).

[16]

RP VARIANTS SER-893 AND THR-893.

RX MEDLINE=21686803; PubMed=11829140; DOI=10.1007/s10038-002-8653-6; Saito S., Iida A., Sekine A., Miura Y., Ogawa C., Kawauchi S., Higuchi S., Nakamura Y.; "Three hundred twenty-six genetic variations in genes encoding nine members of ATP-binding cassette, subfamily B (ABCB/MDR/TAP), in the Japanese population." *J. Hum. Genet.* 47:38-50 (2002).

RL J. Hum. Genet. 47:38-50 (2002).

CC -!- FUNCTION: Energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells.

CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in liver, kidney, small intestine and brain.

CC -!- POLYMORPHISM: Genetic variation in ABCB1 may play a role in patients who do not respond to drug treatment.

CC -!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.

CC -!- SIMILARITY: Contains 2 ABC transmembrane type-1 domains.

CC -!- SIMILARITY: Contains 2 ABC transporter domains.

CC -!- CAUTION: Ref.5 (AAB69423) sequence differs from that shown due to erroneous gene model prediction.

CC -!- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PGY1D105.html".

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

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EMBL: M14758; AAA59575.1; -; mRNA.

EMBL: M29447; AAA59576.1; -; Genomic DNA.

EMBL: M29424; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29425; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29426; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29427; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29428; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29429; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29430; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29431; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29432; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29433; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29434; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29435; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29436; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29437; AAA59576.1; JOINED; Genomic DNA.

EMBL: M29438; AAA59576.1; JOINED; Genomic DNA.

Query Match 96.4%; Score 6212.5; DB 1; Length 1280;

Best Local Similarity 96.5%; Pred No. 2.1e-309;

Matches 1238; Conservative 18; Mismatches 24; Indels 3; Gaps 1;

QY 1 MDLEGRNGAGKQKQFFKLNNKSKDKKERKPTVSFMSFYSNWLKLYMVVGTLLAII 60

Db 1 MDLEGRNGAGKQKQFFKLNNKSKDKKERKPTVSFMSFYSNWLKLYMVVGTLLAII 60

QY 61 HGAGLPMLMLVFGDMTDTFANAGNLGDLGALLFNNTNSNIITDTPVNMLEDMTYAY 120

Db 61 HGAGLPMLMLVFGDMTDTFANAGNLGDLGALLFNNTNSNIITDTPVNMLEDMTYAY 117

QY 121 YSGIGAGVLVAAYIOVSFWCLAAAGQIHKIQKFPHAIMRQEIFGDFVHDVGLNTRLTD 180

Db 118 YSGIGAGVLVAAYIOVSFWCLAAAGQIHKIQKFPHAIMRQEIFGDFVHDVGLNTRLTD 177

QY 181 DYSKINEGIDGKIGMFFQSMATFFFTGIVGFTGRGKLTIVILAISPVGLSAAVWAKILS 240

Db 178 DYSKINEGIDGKIGMFFQSMATFFFTGIVGFTGRGKLTIVILAISPVGLSAAVWAKILS 237

QY 241 SFTDKELLAYAKAGAVAEVLAARTVIAFGQCKKELERYNKLNLEBAKIGIKKAITANI 300

Db 238 SFTDKELLAYAKAGAVAEVLAARTVIAFGQCKKELERYNKLNLEBAKIGIKKAITANI 297

QY 301 STGAFLLIYASVALAFWGTTLTVLSKEYSIGQVLTFRFVSGLIGAFSVGOASPSIEAFAN 360

Db 298 STGAFLLIYASVALAFWGTTLTVLSKEYSIGQVLTFRFVSGLIGAFSVGOASPSIEAFAN 357

QY 361 ARGAAFEIFKIIDNKPISDYSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNKV 420

| | | | |
|------|----|--|------|
| 358 | Db | ARGAAYBEIFKIIDNKPISDYSKSGHKPDNIKGNLEFRNVHFSVPSRKVKILKGLNLKV | 417 |
| 421 | Qy | QSGQTALVGNSGCGKSTTVQLMORLYDPTEGMVSDGQDITRTINNVFLREIIGVWSQEP | 480 |
| 418 | Db | QSGQTALVGNSGCGKSTTVQLMORLYDPTEGMVSDGQDITRTINNVFLREIIGVWSQEP | 477 |
| 481 | Qy | VLPAITTAENIRYGREVDWDETEKAVKEANAYDFIMKLPOKFPDTLVGERGAQLSGGQKQ | 540 |
| 478 | Db | VLPAITTAENIRYGRENVWDETEKAVKEANAYDFIMKLPHKFPDTLVGERGAQLSGGQKQ | 537 |
| 541 | Qy | RIATAARALVZNPKILLDEATSALDTESEAVVOVALDKARKGRITTVIAHRLSVTRNADV | 600 |
| 538 | Db | RIATAARALVZNPKILLDEATSALDTESEAVVOVALDKARKGRITTVIAHRLSVTRNADV | 597 |
| 601 | Qy | IAGFDDGCVIVBEKGNHDELMEKEGYIFKLVTMOTAGNEIELENADESKSEIDTLEMSSH | 660 |
| 598 | Db | IAGFDDGCVIVBEKGNHDELMEKEGYIFKLVTMOTAGNEVELENADESKSEIDALEMSND | 657 |
| 661 | Qy | SGSSLIRKSTRSRVRSQGDRLKSLTKKEALDESIPPVSPFWRIMKMLTWMPYFVGVFC | 720 |
| 658 | Db | SRSSLIRKSTRSRVRSQGDRLKSLTKKEALDESIPPVSPFWRIMKMLTWMPYFVGVFC | 717 |
| 721 | Qy | AIINGGLOPAFANVFSKIIIGIFTRNDAAETKRONSNLPSILLFLVLGIVSITTFPLOGFTF | 780 |
| 718 | Db | AIINGGLOPAFANVFSKIIIGVFTRIDDPETKRONSNLPSILLFLGALGIIISITTFPLOGFTF | 777 |
| 781 | Qy | GKAGEILTKRLVMFVRSMLRQDVSFDDPKNTTGALTTRLANDAAQVKAIGSRLAIIT | 840 |
| 778 | Db | GKAGEILTKRLVMFVRSMLRQDVSFDDPKNTTGALTTRLANDAAQVKAIGSRLAVIT | 837 |
| 841 | Qy | QNTANLGTGIIISIIYQWLTLALLAIVPIIAIAGVVMKMLSGQALKDKKELEGAGKIA | 900 |
| 838 | Db | QNTANLGTGIIISPIYQWLTLALLAIVPIIAIAGVVMKMLSGQALKDKKELEGAGKIA | 897 |
| 901 | Qy | TEAIENRTVVSLTQEQKPFHMYDQSLQVPRNSLRKAHIFGITFSTQAMMFSYAGCF | 960 |
| 898 | Db | TEAIENRTVVSLTQEQKFHYAQSLLQVPRNSLRKAHIFGITFSTQAMMFSYAGCF | 957 |
| 961 | Qy | RFGAYLVAHSIMSPEDVLLVFSAVVFGAMAVGVSSFAPDYAKAKVSAAHIMIEKTPL | 1020 |
| 958 | Db | RFGAYLVAHKUMSPEDVLLVFSAVVFGAMAVGVSSFAPDYAKAKISAAHIIMIEKTPL | 1017 |
| 1021 | Qy | IDSYSTEGKLKNTLEGNVTNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVGSSGCGKS | 1080 |
| 1018 | Db | IDSYSTEGKLKNTLEGNVTGEVFNYPTRDIPVLQGLSLEVKKGQTLALVGSSGCGKS | 1077 |
| 1081 | Qy | TVVOLLRRFYDPLAGKVLDDGKEIKQLNVQMLRAHLGIVSOEPIFLPCDSISENTAYDGN | 1140 |
| 1078 | Db | TVVOLLRRFYDPLAGKVLDDGKEIKRLNVQMLRAHLGIVSOEPIFLPCDSIAENTAYDGN | 1137 |
| 1141 | Qy | RVWSQEEIVRAAKENAHIAFTESIPNKYSTRTVGDKGTQLSGGQKORTAIARALVRQPHIL | 1200 |
| 1138 | Db | RVWSQEEIVRAAKENAHIAFTESIPNKISTKVGDKGTQLSGGQKORTAIARALVRQPHIL | 1197 |
| 1201 | Qy | LLDEATSALDTESEKVVQEALDKAREGRTICIVIAHRLSTIQNADLIIVVFQNGRVEKHGTH | 1260 |
| 1198 | Db | LLDEATSALDTESEKVVQEALDKAREGRTICIVIAHRLSTIQNADLIIVVFQNGRVEKHGTH | 1257 |
| 1261 | Qy | QOLLAQKGIYFSMVSVQAGKRO | 1283 |
| 1258 | Db | QOLLAQKGIYFSMVSVQAGTKRO | 1280 |

OC Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bootth-Genthe C.L., Roller C.R., Rushmore T.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY582533; AAS91647.1; -; mRNA.
DR Ensembl; ENSGCR0000001835; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042826; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR0033593; AAA ATPase.
DR InterPro; IPR011527; ABC_TM_1.
DR InterPro; IPR011140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00664; ABC membrane; 2.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00929; ABC_TM1P; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
DR ATP-binding; Membrane; Nucleotide-binding; Repeat; Transport.
KW GO SEQUENCE 1281 AA, 141634 MW; 7832F50A11334436 CRC64;
SO

| Query Match | 91.1% | Score 5869.5 | DB 2 | Length 1281 |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 90.5% | Pred. No. 7.9e-292 | | |
| Matches 1167 | Conservative 56 | Mismatches 51 | Indels 15 | Gaps 5 |
| Qy | 1 | MDLEGDNGAEKKNPFLANKSKK-DKKERKPTVSVFSMFRYSNWLDDKLYMVVGTAAI | 59 | |
| Db | 1 | MDPEGGKRGAE-KNFWMGKGKKNKEKKKPTVSTFAMFRYSNWLDRLYMLVGTWAAI | 59 | |
| Qy | 60 | IHGAGLPLMWLVFGDMTDTFANAGNLGDLGALLFNNT-----NSSNTIDTVPVNN-LEED | 113 | |
| Db | 60 | IHGALPLMWLVFGNMTDTSFANAG-----ISRNKTFPVIINESITNNTQHFNLHEE | 112 | |
| Qy | 114 | MTRYATYSIGIGAGLVAAAYIOVSFWCLAAAGROIHKIRKOFHAIMRQEIWGFVDVHDVGE | 173 | |
| Db | 113 | MTTVAYYSIGIGAGLVAAAYIOVSFWCLAAAGROIHKIRKOFHAIMRQEIWGFVDVHDVGE | 172 | |
| Qy | 174 | LNTRLTDVSKINEGIGDKIGMFQSQMATPFTGFIIVGFTRGWKLTLVILAIISPVLGSA | 233 | |
| Db | 173 | LNTRLTDVSKINEGIGDKIGMFQSIATPFTGFIIVGFTRGWKLTLVILAIISPVLGSA | 232 | |
| Qy | 234 | VWAKILSSPTDKELLAYAKAGAAVEALAIRTVIAFGGKKELERNKNLNEAKRIGIK | 293 | |
| Db | 233 | IWAKILSSPTDKELLAYAKAGAAVEALAIRTVIAFGGKKELERNKNLNEAKRIGIK | 292 | |
| Qy | 294 | KAITANISIGAAFLIIYASALAPWYGTTLVLKEYSIGQVLTVFFSVLIGAFSGQASP | 353 | |
| Db | 293 | KAITANISIGAAFLIIYASALAPWYGTSLVLSEYSIGQVLTVFFSVLIGAFSGQASP | 352 | |
| Qy | 354 | SIEFAPANARGAAPEIFKIIDNKPSIDSYSKSGHKPNKIGNLFRNVHFSYPSRKEVKIL | 413 | |
| Db | 353 | SIEFAPANARGAAPEIFKIIDNKPSIDSYSKSGHKPNKIGNLFRNVHFSYPSRKEVKIL | 412 | |
| Qy | 414 | KGLNLKVSQGTVALVGNSCGKSTTVQLMORLYDPTPEGMVSVGDQIRNTINVRFLREI | 473 | |
| Db | 413 | KGLNLKVSQGTVALVGNSCGKSTTVQLMORLYDPTDGMVCIDGQIRNTINVRHLREIT | 472 | |
| Qy | 474 | GWVSQEPVLPAITTAENIRYGRBDVTWDETEKAVKEANAVIDFMKLPQKEDTILVBERGAQ | 533 | |

QY 1 MDLEGRNGGAEKKNFFKLNKSKKDKKERTVSVFMSFRYSNWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAEKKNFFKLNKSKKDKKERTVSVFMSFRYSNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTRYAY 117
QY 121 YSGIGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMROEIGFVDHVGELNTRLTD 180
DB 118 YSGIGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMROEIGFVDHVGELNTRLTD 177
QY 181 DVSKINEGIGDKIGNFFQSMATFFTGFIPTGTRGKMLTLVILAIISPVGLSAAVWAKILS 240
DB 178 DVSKINEGIGDKIGNFFQSMATFFTGFIPTGTRGKMLTLVILAIISPVGLSAAVWAKILS 237
QY 241 SFTDKELLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNNKLEBEAKRIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNNKLEBEAKRIGIKKAITANI 297
QY 301 SIGAFLIYASYALAFWYGTITLVLSKEYSIGOVLTVPFSLVIGAPSVGOASPSIEAFAN 360
DB 298 SIGAFLIYASYALAFWYGTITLVLSKEYSIGOVLTVPFSLVIGAPSVGOASPSIEAFAN 357
QY 361 ARGAAFEIKIDNKPSIDSYSGHKKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKV 420
DB 358 ARGAAFEIKIDNKPSIDSYSGHKKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKV 417
QY 421 QSGQTVLVGNSGCGKSTTVQMLQRLYDPTGEMVSDGQDINTINVRFLREIIGVVSQBP 480
DB 418 QSGQTVLVGNSGCGKSTTVQMLQRLYDPTGEMVSDGQDINTINVRFLREIIGVVSQBP 477
QY 481 VLFATTIAENTRYGREDVTMDIEKAVKEANAYDTIMKLPQKFDTLGGERGAQLSGGQK 540
DB 478 VLFATTIAENTRYGREDVTMDIEKAVKEANAYDTIMKLPQKFDTLGGERGAQLSGGQK 537
QY 541 RIATARALVRNPKILLDEATSEAVVQVALDKARKGRITIVIAHRLSTVRNADV 600
DB 538 RIATARALVRNPKILLDEATSEAVVQVALDKARKGRITIVIAHRLSTVRNADV 597
QY 601 IAGFDGVIYVEKGNHDELMKEGIYFKLVMTQAGNEIELENADESKSEIDTLESSH 660
DB 598 IAGFDGVIYVEKGNHDELMKEGIYFKLVMTQAGNEIELENADESKSEIDTLESSH 657
QY 661 SGSSLIIRKSTRSRRSGGQDRKLSKEALDESIPPVSWFMKMLNLTWFFVGVFC 720
DB 658 SGSSLIIRKSTRSRRSGGQDRKLSKEALDESIPPVSWFMKMLNLTWFFVGVFC 717
QY 721 AIINGLOPAPAVIFSKIIIGIFTRNDDAETKQNSNLFSLFLVLGIVSFIFFLQGTFF 780
DB 718 AIINGLOPAPAVIFSKIIIGIFTRNDDAETKQNSNLFSLFLVLGIVSFIFFLQGTFF 777
QY 781 KGAGILTRURMYFRSMLRDVSWFDDPKNTTGALTTRLANDAAQVKGALGSLAIIT 840
DB 778 KGAGILTRURMYFRSMLRDVSWFDDPKNTTGALTTRLANDAAQVKGALGSLAIIT 837
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DB 838 QNIANLGTGIIISLYGQWLTLLAIIPVILAIAGVVENKMLSGQALDKKLEGAAGKIA 897
QY 901 TEAIENFRVTVSLTQEQFEHMYDQSLQVPYRNSLRKAHIFGITSFTQAMMYFSYAGCF 960
DB 898 TEAIENFRVTVSLTQEQFEHMYDQSLQVPYRNSLRKAHIFGITSFTQAMMYFSYAGCF 957
QY 961 RFGAYLVHSLMSFEDVLLVPSAVVFGAMAVGQVSSPADYAKAKVSAAHIIIMIEKTP 1020
DB 958 RFGAYLVHSLMSFEDVLLVPSAVVFGAMAVGQVSSPADYAKAKVSAAHIIIMIEKTP 1017
QY 1021 IDSYSTEGIKPNTLGNVTNFWFNYPTRLDIPVLOGLSLEVKGGOTLALVSGSGCGKS 1080
DB 1018 IDSYSTEGIKPNTLGNVTNFWFNYPTRLDIPVLOGLSLEVKGGOTLALVSGSGCGKS 1077
QY 1081 TVVQLLERYFDPLAGKVLDDGKEIKQLNVQWLAHGLIVSOPPIILFDCSISENIAYGNS 1140

DB 1078 TVVQLLERYFDPLAGKVLDDGKEIKQLNVQWLAHGLIVSOPPIILFDCSISENIAYGNS 1137
QY 1141 RVVQEEIVRAAKANIHAFIESLPNKYSTVTRVGDKGTQLSGGQKORIAARALVRQPHIL 1200
DB 1138 RVVQEEIVRAAKANIHAFIESLPNKYSTVTRVGDKGTQLSGGQKORIAARALVRQPHIL 1197
QY 1201 LLDATSALDTESEKVVQEALDKAREGRTICIVIAHRLSTIONADLIIVFQNGRVKEHGT 1260
DB 1198 LLDATSALDTESEKVVQEALDKAREGRTICIVIAHRLSTIONADLIIVFQNGRVKEHGT 1257
QY 1261 QOLLAQGIYFMSVSVQAGAKRQ 1283
DB 1258 QOLLAQGIYFMSVSVQAGAKRQ 1280
RESULT 6
US-09-584-586-2
Sequence 2, Application US/09584586
Patent No. 6933150
GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Bunting, Kevin
TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
FILE REFERENCE: 1340-1-021CIP
CURRENT APPLICATION NUMBER: US/09/584,586
CURRENT FILING DATE: 2000-05-31
EARLIER APPLICATION NUMBER: US 60/086,988
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: PCT/US99/11825
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human MDR 185-G
US-09-584-586-2
Query Match 96.4%; Score 6212.5; DB 2; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1238; Conservative 18; Mismatches 24; Indels 3; Gaps 1;
QY 1 MDLEGRNGGAEKKNFFKLNKSKKDKKERTVSVFMSFRYSNWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAEKKNFFKLNKSKKDKKERTVSVFMSFRYSNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTRYAY 117
QY 121 YSGIGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMROEIGFVDHVGELNTRLTD 180
DB 118 YSGIGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMROEIGFVDHVGELNTRLTD 177
QY 181 DVSKINEGIGDKIGNFFQSMATFFTGFIPTGTRGKMLTLVILAIISPVGLSAAVWAKILS 240
DB 178 DVSKINEGIGDKIGNFFQSMATFFTGFIPTGTRGKMLTLVILAIISPVGLSAAVWAKILS 237
QY 241 SFTDKELLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNNKLEBEAKRIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAVAEVLAAIRTVIAFGGQKKELERYNNKLEBEAKRIGIKKAITANI 297
QY 301 SIGAFLIYASYALAFWYGTITLVLSKEYSIGOVLTVPFSLVIGAPSVGOASPSIEAFAN 360
DB 298 SIGAFLIYASYALAFWYGTITLVLSKEYSIGOVLTVPFSLVIGAPSVGOASPSIEAFAN 357
QY 361 ARGAAFEIKIDNKPSIDSYSGHKKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKV 420
DB 358 ARGAAFEIKIDNKPSIDSYSGHKKPDNIKGNLEFRNVHPSYPSRKEVKILKGLNKV 417

421 QSGQTVLVGSGCGKSTTVQMLQRLYDPTGKMSVSDGDIPTINVRFLREIIGVVSQEP 480
418 QSGQTVLVGSGCGKSTTVQMLQRLYDPTGKMSVSDGDIPTINVRFLREIIGVVSQEP 477
481 VLPATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGQALSGGQKQ 540
478 VLPATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGQALSGGQKQ 537
541 RIAIARALVRNPKILLDEATSDALDTESEAVVQVADLKARKGRTTIVIAHRLSTVRNADV 600
538 RIAIARALVRNPKILLDEATSDALDTESEAVVQVADLKARKGRTTIVIAHRLSTVRNADV 597
601 IAGFDGVIYKGNHDELMEKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSSHD 660
598 IAGFDGVIYKGNHDELMEKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSSHD 657
661 SGSSLIIRKSTRRSVRGSGQDRKSLSTKEALDESIPPVSFWRMKLNLTWEPYFVVGVC 720
658 SRSSLIIRKSTRRSVRGSGQDRKSLSTKEALDESIPPVSFWRMKLNLTWEPYFVVGVC 717
721 AIINGLOPAPAVIFSKIIIGIIFTRNDDEATKQNSNLFSLFLVLGIVSFIITFFLOGTF 780
718 AIINGLOPAPAVIFSKIIIGIIFTRNDDEATKQNSNLFSLFLVLGIVSFIITFFLOGTF 777
781 GKAGEILTKRLRYMFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSLRLAIT 840
778 GKAGEILTKRLRYMFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSLRLAIT 837
841 QNIANLGTGIIISLIYGMWLTLLLAIVPTIALAGVVENKMLSGQALDKKCELEGAGKIA 900
838 QNIANLGTGIIISLIYGMWLTLLLAIVPTIALAGVVENKMLSGQALDKKCELEGAGKIA 897
901 TEAIENFRVTSITQOKFHEMYDQSLQVPRYNSLRKAHIFGITPFTQAMVYFSYAGCF 960
898 TEAIENFRVTSITQOKFHEMYDQSLQVPRYNSLRKAHIFGITPFTQAMVYFSYAGCF 957
961 RFGAYLVANSLMSPEDVLLVFSVAVFGMAVGVSSFPADYAKAKVSAHIIMIIEKTPL 1020
958 RFGAYLVANSLMSPEDVLLVFSVAVFGMAVGVSSFPADYAKAKVSAHIIMIIEKTPL 1017
1021 IDSYSTGLKPNTEGNTVFNVEVFNPTLDPVLQGLSLEVKKGQTLALVSSGCGKS 1080
1018 IDSYSTGLKPNTEGNTVFNVEVFNPTLDPVLQGLSLEVKKGQTLALVSSGCGKS 1077
1081 TVVOLLERFYDPLAGKVLDDGKEIKOLNVOMLRAHLGIVSQBPILFDCSISENIAVDNS 1140
1078 TVVOLLERFYDPLAGKVLDDGKEIKOLNVOMLRAHLGIVSQBPILFDCSISENIAVDNS 1137
1141 RVYSQBEIVRAAKENHAFIESIPNKYSTVGVGDKGTQLSGQKQRIARALVRQPHIL 1200
1138 RVYSQBEIVRAAKENHAFIESIPNKYSTVGVGDKGTQLSGQKQRIARALVRQPHIL 1197
1201 LLDDEATSDALDTESEKVVQVQALDKAREGRTCVIAHRLSTTIONADLIYVFNQGRVKEHGH 1260
1198 LLDDEATSDALDTESEKVVQVQALDKAREGRTCVIAHRLSTTIONADLIYVFNQGRVKEHGH 1257
1261 QQLLAQKGIYFMSVVOAGTKRQ 1283
1258 QQLLAQKGIYFMSVVOAGTKRQ 1280

RESULT 7
US-09-767-594-2
Sequence 2, Application US/09767594
Patent No. 6521635
GENERAL INFORMATION:
APPLICANT: Bates, Susan
APPLICANT: Robey, Robert
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

FILE REFERENCE: 015280-402100US
CURRENT APPLICATION NUMBER: US/09/767,594
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 60/177,410
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
OTHER INFORMATION: protein
US-09-767-594-2
Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
QY 1 MDLEGRNGGAEKKNFFKLNKSKDKKERKPTVSVFSMFRYSNWLKLYMVVGTLLAAII 60
DB 1 MDLEGRNGGAEKKNFFKLNKSKDKKERKPTVSVFSMFRYSNWLKLYMVVGTLLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNTHSSNITDTPVNMLEEDMTRVAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNTHSSNITDTPVNMLEEDMTRVAY 117
QY 121 YSGIGAGTVAAAYIQVSWFCLAAAGROHKKIRKQFPHAIKQFHWDFVHDVGEINLRLTD 180
DB 118 YSGIGAGTVAAAYIQVSWFCLAAAGROHKKIRKQFPHAIKQFHWDFVHDVGEINLRLTD 177
QY 181 DVSKINEGIGKIGKIFFQSMATFFTFIVGTRGKGLTLVLAISPVGLSAAVWAKTILS 240
DB 178 DVSKINEGIGKIGKIFFQSMATFFTFIVGTRGKGLTLVLAISPVGLSAAVWAKTILS 237
QY 241 SPTDKELLAYAKAGAVAEVLAARTVIAFGOKKELERYNKNLEAKRIGIKKAITANI 300
DB 238 SPTDKELLAYAKAGAVAEVLAARTVIAFGOKKELERYNKNLEAKRIGIKKAITANI 297
QY 301 SIGAFLIYASALAFWYGTTLVLSKEYSIGQVLTFFSVLIGAFSQAQSPSIEAFAN 360
DB 298 SIGAFLIYASALAFWYGTTLVLSKEYSIGQVLTFFSVLIGAFSQAQSPSIEAFAN 357
QY 361 ARGAAFEIPIKIDNKPSIDSYSGKHKPDNIGKLEFRNVHFSYPSRKEVKILKGLNLKV 420
DB 358 ARGAAFEIPIKIDNKPSIDSYSGKHKPDNIGKLEFRNVHFSYPSRKEVKILKGLNLKV 417
QY 421 QSGQTVLVGSGCGKSTTVQMLQRLYDPTGKMSVSDGDIPTINVRFLREIIGVVSQEP 480
DB 418 QSGQTVLVGSGCGKSTTVQMLQRLYDPTGKMSVSDGDIPTINVRFLREIIGVVSQEP 477
QY 481 VLPATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGQALSGGQKQ 540
DB 478 VLPATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGQALSGGQKQ 537
QY 541 RIAIARALVRNPKILLDEATSDALDTESEAVVQVADLKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RIAIARALVRNPKILLDEATSDALDTESEAVVQVADLKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGFDGVIYKGNHDELMEKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSSHD 660
DB 598 IAGFDGVIYKGNHDELMEKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSSHD 657
QY 661 SGSSLIIRKSTRRSVRGSGQDRKSLSTKEALDESIPPVSFWRMKLNLTWEPYFVVGVC 720
DB 658 SRSSLIIRKSTRRSVRGSGQDRKSLSTKEALDESIPPVSFWRMKLNLTWEPYFVVGVC 717
QY 721 AIINGLOPAPAVIFSKIIIGIIFTRNDDEATKQNSNLFSLFLVLGIVSFIITFFLOGTF 780
DB 718 AIINGLOPAPAVIFSKIIIGIIFTRNDDEATKQNSNLFSLFLVLGIVSFIITFFLOGTF 777

| | | | | | |
|-----------------------|------------------|--|-----------|--------------|--|
| Query Match | 96.3%; | Score 6203.5; | DB 2; | Length 1280; | |
| Best Local Similarity | 96.4%; | Pred. No. 0; | | | |
| Matches 1237; | Conservative 18; | Mismatches 25; | Indels 3; | Gaps 1; | |
| QY | 1 | MDLEGDRNGAEGKKNFKLNKSKKKKKKPTVSFVSFMYRNWLDKLYMVVGTAAII | 60 | | |
| DB | 1 | MDLEGDRNGAEGKKNFKLNKSKKKKKKPTVSFVSFMYRNWLDKLYMVVGTAAII | 60 | | |
| QY | 61 | HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAY | 120 | | |
| DB | 61 | HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAY | 117 | | |
| QY | 121 | YSGIGAGLVAAVYQVSWFCLAAAGQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD | 180 | | |
| DB | 118 | YSGIGAGLVAAVYQVSWFCLAAAGQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD | 177 | | |
| QY | 181 | DVSKINEGIGDKIGMFPQSMATPFTGIVGTGKWLTLVLAISPVGLSAAVWAKILS | 240 | | |
| DB | 178 | DVSKINEGIGDKIGMFPQSMATPFTGIVGTGKWLTLVLAISPVGLSAAVWAKILS | 237 | | |
| QY | 241 | SFTDKELLAYAKAGAVAEVLAIRTIVAFGGQKELERNKNLEAKRIGIKAITANI | 300 | | |
| DB | 238 | SFTDKELLAYAKAGAVAEVLAIRTIVAFGGQKELERNKNLEAKRIGIKAITANI | 297 | | |
| QY | 961 | RFAGYLVAHSLMSFEDVLVFSVAVFGMAVGVSSPAPDYAKAKVSAHHIMIEKTP | 1020 | | |
| DB | 958 | RFAGYLVAHSLMSFEDVLVFSVAVFGMAVGVSSPAPDYAKAKVSAHHIMIEKTP | 1017 | | |
| QY | 1021 | IDSYSTEGKLPNTLEGNVTTFNEVFNYPTRLDIPVLQGLSLEVKGQTLALVSSGCGKS | 1080 | | |

| | | | | | |
|---|------|--|------|--|--|
| DB | 1018 | IDSYSTEGKLPNTLEGNVTTFNEVFNYPTRLDIPVLQGLSLEVKGQTLALVSSGCGKS | 1077 | | |
| QY | 1081 | TVVQLLEFPYDPLAGKVLDDGKEIKQLNVQWLRHLGIVSQEPILFDCSISENTAYGNS | 1140 | | |
| DB | 1078 | TVVQLLEFPYDPLAGKVLDDGKEIKQLNVQWLRHLGIVSQEPILFDCSISENTAYGNS | 1137 | | |
| QY | 1141 | RVSQEEIVRAAKENIHAFTESLPNKYSTVGVKGTQSGOKORIAIARALVRQPHIL | 1200 | | |
| DB | 1138 | RVSQEEIVRAAKENIHAFTESLPNKYSTVGVKGTQSGOKORIAIARALVRQPHIL | 1197 | | |
| QY | 1201 | LDDEATSDLTSEKVVQSDALDKAREGRTCVIAHRLSTIQNADLIVVFQNGRVEHGH | 1260 | | |
| DB | 1198 | LDDEATSDLTSEKVVQSDALDKAREGRTCVIAHRLSTIQNADLIVVFQNGRVEHGH | 1257 | | |
| QY | 1261 | QQLLAQKGIYFSMVSVQAGAKRQ | 1283 | | |
| DB | 1258 | QQLLAQKGIYFSMVSVQAGAKRQ | 1280 | | |
| RESULT 11 | | | | | |
| US-09-817-762-3 | | | | | |
| Sequence 3, Application US/09817762 | | | | | |
| Patent No. 6858774 | | | | | |
| GENERAL INFORMATION | | | | | |
| APPLICANT: Spalding, Edgar P. | | | | | |
| APPLICANT: No. 6858774, Bosh | | | | | |
| TITLE OF INVENTION: MDR-Like ABC Transporter Gene From | | | | | |
| TITLE OF INVENTION: Plants | | | | | |
| FILE REFERENCE: 13238-00061 | | | | | |
| CURRENT APPLICATION NUMBER: US/09/817,762 | | | | | |
| CURRENT FILING DATE: 2001-03-26 | | | | | |
| PRIOR APPLICATION NUMBER: PCT/US99/22363 | | | | | |
| PRIOR FILING DATE: 1999-09-24 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/101,814 | | | | | |
| PRIOR FILING DATE: 1998-09-25 | | | | | |
| NUMBER OF SEQ ID NOS: 14 | | | | | |
| SOFTWARE: FASTSEQ for Windows Version 4.0 | | | | | |
| SEQ ID NO 3 | | | | | |
| LENGTH: 1280 | | | | | |
| TYPE: PRT | | | | | |
| ORGANISM: Homo sapiens | | | | | |
| PUBLICATION INFORMATION: | | | | | |
| DATABASE ACCESSION NUMBER: Genbank P08183 | | | | | |
| DATABASE ENTRY DATE: 1997-11-01 | | | | | |
| US-09-817-762-3 | | | | | |
| Query Match 96.3%; Score 6203.5; DB 2; Length 1280; | | | | | |
| Best Local Similarity 96.4%; Pred. No. 0; | | | | | |
| Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1; | | | | | |
| QY | 1 | MDLEGDRNGAEGKKNFKLNKSKKKKKKPTVSFVSFMYRNWLDKLYMVVGTAAII | 60 | | |
| DB | 1 | MDLEGDRNGAEGKKNFKLNKSKKKKKKPTVSFVSFMYRNWLDKLYMVVGTAAII | 60 | | |
| QY | 61 | HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAY | 120 | | |
| DB | 61 | HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVPMLEEDMTYAY | 117 | | |
| QY | 121 | YSGIGAGLVAAVYQVSWFCLAAAGQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD | 180 | | |
| DB | 118 | YSGIGAGLVAAVYQVSWFCLAAAGQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD | 177 | | |
| QY | 181 | DVSKINEGIGDKIGMFPQSMATPFTGIVGTGKWLTLVLAISPVGLSAAVWAKILS | 240 | | |
| DB | 178 | DVSKINEGIGDKIGMFPQSMATPFTGIVGTGKWLTLVLAISPVGLSAAVWAKILS | 237 | | |
| QY | 241 | SFTDKELLAYAKAGAVAEVLAIRTIVAFGGQKELERNKNLEAKRIGIKAITANI | 300 | | |
| DB | 238 | SFTDKELLAYAKAGAVAEVLAIRTIVAFGGQKELERNKNLEAKRIGIKAITANI | 297 | | |
| QY | 301 | SIGAAFLIYASALAFWYGTTLVLSKEYSIGQVLTVPFVSVLGAQVSGQSKQ | 360 | | |

298 SIGAAFLIYASALAFWYGTTLVLSGEYSIGQVLTVPFVSLVIGAFVSGQASPSIEAFAN 357
361 ARGAAPEIFKIIDNKPSIDTSYKSGHKPDNKGLEPRNVHFSYPSRKEVKILKGLNLKV 420
358 ARGAAPEIFKIIDNKPSIDTSYKSGHKPDNKGLEPRNVHFSYPSRKEVKILKGLNLKV 417
421 QSGQTVLAVGNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBP 480
418 QSGQTVLAVGNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBP 477
481 VLPATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGQK 540
478 VLPATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGQK 537
541 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
538 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
601 IAGPDDGVIVKGNHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDTLEMSSHD 660
598 IAGPDDGVIVKGNHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDALEMSSND 657
661 SGSSLIKRSTRSRVRSVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPFYFVGVFC 720
658 SRSSLIKRSTRSRVRSVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPFYFVGVFC 717
721 AIINGGLQPAFAVIFSKIIIGITFRNDDAETKRONSLFSLFLVIGIVSFITFLQGF 780
718 AIINGGLQPAFAVIFSKIIIGITFRNDDAETKRONSLFSLFLVIGIVSFITFLQGF 777
781 KGAELTKRLRYMVFRSMQLQDVSFDDPKNTGALTTRLANDAAQVKGAGISRLAIT 840
778 KGAELTKRLRYMVFRSMQLQDVSFDDPKNTGALTTRLANDAAQVKGAGISRLAIT 837
841 QNIANLGTGIIISLYGQHLTLLAIIVPIIAIGVEMKMLSGQALKDKELEGAKIA 900
838 QNIANLGTGIIISLYGQHLTLLAIIVPIIAIGVEMKMLSGQALKDKELEGAKIA 897
901 TEAIENFRVTVSLTQEQKFEHMYQSLQVPRYNSLRKAHIFGITPFTQAMMYPSYAGCF 960
898 TEAIENFRVTVSLTQEQKFEHMYQSLQVPRYNSLRKAHIFGITPFTQAMMYPSYAGCF 957
961 RFGAYLVAHLSMEDVLLVFSVAVFGAMVQVSSFPADYAKAKISAAHIIIMIEKTPL 1020
958 RFGAYLVAHLSMEDVLLVFSVAVFGAMVQVSSFPADYAKAKISAAHIIIMIEKTPL 1017
1021 IDSYSTGLKENTLEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSGSGGCKS 1080
1018 IDSYSTGLKENTLEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSGSGGCKS 1077
1081 TVVOLLERFYDPLAGKVLDDKEIKQLNVOMLRAHLGIVSOEPILFDCSISENTAYGDSN 1140
1078 TVVOLLERFYDPLAGKVLDDKEIKQLNVOMLRAHLGIVSOEPILFDCSISENTAYGDSN 1137
1141 RVVSOEIVRAAKENIHAFTESLPNKYSTYTRVGDGTOLSGQOKORIAIARALVRQPHIL 1200
1138 RVVSOEIVRAAKENIHAFTESLPNKYSTYTRVGDGTOLSGQOKORIAIARALVRQPHIL 1197
1201 LLDATSALDTESEKVVQALDKAREGRTICIVIAHRLSTIONADLIVVFQNGRVEKHGTH 1260
1198 LLDATSALDTESEKVVQALDKAREGRTICIVIAHRLSTIONADLIVVFQNGRVEKHGTH 1257
1261 QOLLAQKGIYFSMVSVOAGKQ 1283
1258 QOLLAQKGIYFSMVSVOAGKQ 1280

RESULT 12
US-09-584-586-4
Sequence 4, Application US/09584586
Patent No. 693150
PUBLICATION INFORMATION:
INVENTOR: Sorrentino, Brian

APPLICANT: Bunting, Kevin
TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
FILE REFERENCE: MDR-1 METHODS OF USE THEREOF
CURRENT FILING DATE: 2000-05-31
EARLIER FILING DATE: 1998-05-28
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human MDR 185-V
US-09-584-586-4
Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
QY 1 MDLEGDRNGAEGKKNPFKLNKSKDKKPKPTVSFMSFRYSNMLDKLYMVVGTAAII 60
DB 1 MDLEGDRNGAEGKKNPFKLNKSKDKKPKPTVSFMSFRYSNMLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSSNITDTVPVNMLEBDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSSNITDTVPVNMLEBDMTRYAY 117
QY 121 YSGIGAGLVAAIYQVSPWCLAAGROIHKIQOFHAIMRQEIHWDFDHDVHDELNRLTD 180
DB 118 YSGIGAGLVAAIYQVSPWCLAAGROIHKIQOFHAIMRQEIHWDFDHDVHDELNRLTD 177
QY 181 DVSKINEGIDKIMGFQSMATPFTGFIYVGRGWKLTILVLAISPVLSAAVAKILS 240
DB 178 DVSKINEGIDKIMGFQSMATPFTGFIYVGRGWKLTILVLAISPVLSAAVAKILS 237
QY 241 SFTDKELLAYAKAGAVAEVLAIRTVIAPGQKKELRYNKNLEAKRIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAVAEVLAIRTVIAPGQKKELRYNKNLEAKRIGIKKAITANI 297
QY 301 SIGAFLIYASALAFWYGTTLVLSGEYSIGQVLTVPFVSLVIGAFVSGQASPSIEAFAN 360
DB 298 SIGAFLIYASALAFWYGTTLVLSGEYSIGQVLTVPFVSLVIGAFVSGQASPSIEAFAN 357
QY 361 ARGAAPEIFKIIDNKPSIDTSYKSGHKPDNKGLEPRNVHFSYPSRKEVKILKGLNLKV 420
DB 358 ARGAAPEIFKIIDNKPSIDTSYKSGHKPDNKGLEPRNVHFSYPSRKEVKILKGLNLKV 417
QY 421 QSGQTVLAVGNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBP 480
DB 418 QSGQTVLAVGNSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBP 477
QY 481 VLPATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGQK 540
DB 478 VLPATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGQK 537
QY 541 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGPDDGVIVKGNHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDTLEMSSHD 660
DB 598 IAGPDDGVIVKGNHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDALEMSSND 657
QY 661 SGSSLIKRSTRSRVRSVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPFYFVGVFC 720
DB 658 SRSSLIKRSTRSRVRSVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPFYFVGVFC 717
QY 721 AIINGGLQPAFAVIFSKIIIGITFRNDDAETKRONSLFSLFLVIGIVSFITFLQGF 780